

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:08:47 ; Search time 71 Seconds  
(without alignments)  
354,076 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483

Perfect score: 382  
Sequence: 1 DAPANPCDDAATCKLTGSG.....DUDYCNISAGCPNPFHA 65

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	382	100.0	483	3	AA799413 Southern
2	382	100.0	483	4	AAE03036 Agkistrod
3	346	90.6	73	2	AAW14083 Platelet
4	346	90.6	73	3	AAW14083 Platelet
5	346	90.6	73	3	AAW14083 Platelet
6	345	90.3	73	5	AAE19791 Korean sn
7	337	88.2	73	5	AAE19787 Agkistrod
8	334	87.4	73	2	AAE06494 Platelet
9	334	87.4	73	2	AAE06494 Platelet
10	334	87.4	73	2	AAE06494 Platelet
11	334	87.4	73	2	AAE06494 Platelet
12	334	87.4	73	2	AAE06494 Platelet
13	334	87.4	73	2	AAE06494 Platelet
14	334	87.4	73	2	AAE06494 Platelet
15	334	87.4	73	2	AAE06494 Platelet
16	334	87.4	73	2	AAE06494 Platelet
17	334	87.4	73	2	AAE06494 Platelet
18	334	87.4	73	2	AAE06494 Platelet
19	334	87.4	73	2	AAE06494 Platelet
20	334	87.4	73	2	AAE06494 Platelet
21	334	87.4	73	2	AAE06494 Platelet
22	334	87.4	73	2	AAE06494 Platelet
23	334	87.4	73	2	AAE06494 Platelet
24	334	87.4	73	2	AAE06494 Platelet
25	334	87.4	73	2	AAE06494 Platelet

26	325	85.1	106	2	AAE25152 Bifunctio
27	323	84.6	73	2	ADP65996 Snake ven
28	322	84.3	72	2	AAE10109 Trigramin
29	322	84.3	97	2	AAE28705 Bifunctio
30	322	84.3	97	2	AAE28705 Bifunctio
31	322	84.3	98	2	AAE28708 Bifunctio
32	322	84.3	98	2	AAE25154 Bifunctio
33	321.5	84.3	71	5	AAE25150 Bifunctio
34	319.5	83.6	71	5	AAE25152 Bifunctio
35	319	83.5	96	2	AAE25151 Bifunctio
36	319	83.5	96	2	AAE25151 Bifunctio
37	319	83.5	96	2	AAE25151 Bifunctio
38	318	83.2	72	1	AAE25147 Bifunctio
39	307.5	80.5	73	2	AAE25147 Bifunctio
40	307	80.4	72	2	AAE25147 Bifunctio
41	302	79.1	73	6	ABP97448 Disintegr
42	301.5	78.9	71	2	ADP66000 Snake ven
43	288	75.4	73	6	ADP97447 Disintegr
44	287	75.1	72	2	AAW46215 Snake ven
45	287	75.1	72	2	AAW50453 Snake ven

#### ALIGNMENTS

RESULT 1	
AA799413	
ID	AA799413 standard, protein, 483 AA.
AC	AA799413;
XX	
XX	
DT	26-AUG-2004 (revised)
DT	01-AUG-2000 (first entry)
XX	
DE	Southern copperhead snake conortrostatin.
XX	
XX	
KW	Southern copperhead snake; venom; conortrostatin; disintegrin;
KW	cytotoxic; antiproliferative; thrombolytic; cerebroprotective;
KW	antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
KW	thrombolytic; thrombolytic; thrombolytic; thrombolytic; thrombolytic;
KW	embolism; aneurism; angina; myocardial infarction; integrin.
OS	Agkistrodon contortrix.
XX	
XX	Unidentified.
XX	
XX	
FT	Key
FT	Region
FT	Location/Qualifiers
FT	1.190
FT	/note="Pro-region; a protein comprising this region is
FT	separately claimed in Claim 3c"
FT	191.410
FT	/note="Metalloproteinase region; a protein comprising
FT	this region is separately claimed in Claim 3b"
FT	333
FT	/note="Encoded by CCC"
FT	419.483
FT	/note="Conortrostatin monomer; a protein comprising
FT	this region is separately claimed in Claim 3a"
FT	457.469
FT	/note="Peptide loop, includes RGD sequence at residues
FT	461-463; acts as integrin antagonist"
PN	WO200018421-A1.
PD	06-APR-2000.
PF	
PF	29-SEP-1999;
PF	99WO-US022608.
PR	
PR	29-SEP-1998;
PR	98US-00163047.
XX	
XX	(USC) UNIV SOUTHERN CALIFORNIA.
XX	Markland FS, Zhou Q;
XX	
XX	

DR WPI; 2000-303389/26.  
 DR N-PSDB; AA294881.  
 XX  
 PT Novel proteins and polynucleotides representing contortrostatin useful  
 for inhibiting platelet aggregation, tumor metastasis and growth.  
 XX  
 PS Claim 3d; Fig 3A-C; 81pp; English.  
 XX  
 CC The present sequence is that of the Southern copperhead snake venom  
 disintegrin, contortrostatin, a protein that inhibits the interactions  
 between integrins and their receptors. The sequence was deduced from  
 CC isolated snake venom cDNA (see AA294881). The contortrostatin precursor  
 CC protein includes a pro-protein region, a metalloproteinase region which  
 CC includes a metal-binding motif, and a disintegrin region which includes  
 CC an RGD loop that acts as an integrin antagonist. Polypeptides comprising  
 CC the pro-region, the metalloproteinase region, and the contortrostatin  
 CC monomer, as well as the full-length precursor protein, can be obtained  
 CC using recombinant DNA methods. The purified proteins are used in  
 CC pharmaceutical compositions for treating diseases associated with an  
 CC integrin binding to an integrin receptor, especially to inhibit platelet  
 CC aggregation, tumour metastasis, angiogenesis, neovascularization, cell  
 CC adhesion, invasiveness, or growth (all claimed). The proteins are also  
 CC useful for treating a thrombotic disorder, e.g. preventing arterial,  
 CC venous, and microvascular thrombosis and thromboembolism, stroke,  
 CC transient ischaemic attacks, arteriosclerosis, atherosclerosis, pulmonary  
 CC embolism, aneurism, angina and myocardial infarction  
 CC  
 CC Revised record issued on 26-AUG-2004 : Correction to feature table key  
 CC  
 XX  
 SQ Sequence 483 AA;  
 Query Match 100.0%; Score 382; DB 3; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAPANPCDDAATCKLTGSGCADGICCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPR 60  
 DB 419 DAPANPCDDAATCKLTGSGCADGICCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPR 478  
 QY 61 NPFHA 65  
 DB 479 NPFHA 483  
 DB

RESULT 2  
 AA03036  
 ID AA03036 standard; protein; 483 AA.  
 XX  
 AC AA03036;  
 XX  
 DT 04-AUG-2001 (first entry)  
 XX  
 DE Agkistrodon contortrix contortrostatin (CN) protein.  
 XX  
 KW Southern copper head snake; contortrostatin; CN; cytostatic; osteopathic;  
 KW vulnerary; disintegrin; platelet aggregation; neovascularisation; tumour;  
 KW integrin; angiogenesis; metastasis; invasiveness; growth; metastasis;  
 KW melanoma; carcinoma; sarcoma; therapy; thrombotic disease; osteoporosis;  
 KW wound healing.  
 XX  
 OS Agkistrodon contortrix.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..190  
 FT Domain /label= Proprotein  
 FT Domain 191..410  
 FT Binding-site /label= Metalloproteinase  
 FT Binding-site 334..344  
 FT Domain /label= Zinc-binding\_motif  
 FT Domain 419..483  
 FT Region /label= Disintegrin  
 FT Region 424..433  
 FT /label= Conserved\_sequence

FT /note= "This sequence is used for designing PCR primers  
 FT PCR-1 and PCR-2"  
 FT Domain 461..463  
 FT /label= RGD\_sequence  
 XX  
 PN WO200141791-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 09-DEC-2000; 2000WO-US033367.  
 XX  
 PR 10-DEC-1999; 99US-00460295.  
 PR 08-JUN-2000; 2000US-00591552.  
 XX  
 PA (USC-) UNIV SOUTHERN CALIFORNIA.  
 XX  
 PI Markland FS, Zhou Q;  
 XX  
 DR WPI; 2001-381494/40.  
 DR N-PSDB; AAD07386.  
 XX  
 PT Homodimeric disintegrin useful for modulating the adhesion, motility, and  
 PT invasiveness of integrin expressing tumor cells.  
 XX  
 PS Claim 12; Fig 3; 101pp; English.  
 XX  
 CC The present sequence is contortrostatin (CN) protein from southern copper  
 CC head snake. CN, a homodimeric disintegrin binds to integrin alphavbeta5  
 CC and induces alphavbeta5-mediated tyrosine phosphorylation of CAs and FAK  
 CC in tumor cells. CN is useful for modulating the adhesion, motility, and  
 CC invasiveness of integrin expressing cells, preferably tumor cells and  
 CC for inhibiting the adhesion of integrin expressing cells to vitronectin.  
 CC The pharmaceutical composition comprising CN is useful for inhibiting  
 CC platelet aggregation, neovascularisation, angiogenesis, tumour  
 CC metastasis, invasiveness or growth, for inhibiting metastasis in  
 CC melanoma, carcinoma and sarcoma patients. It is also useful for treating  
 CC thrombotic diseases, osteoporosis, and wound healing in mammals  
 CC  
 XX  
 SQ Sequence 483 AA;  
 Query Match 100.0%; Score 382; DB 4; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-29;  
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAPANPCDDAATCKLTGSGCADGICCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPR 60  
 DB 419 DAPANPCDDAATCKLTGSGCADGICCDQCKFMKEGTVCRARAGDDDDYCNGISAGCPR 478  
 QY 61 NPFHA 65  
 DB 479 NPFHA 483  
 DB

RESULT 3  
 AAW14083  
 ID AAW14083 standard; peptide; 73 AA.  
 XX  
 AC AAW14083;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 27-OCT-1997 (first entry)  
 XX  
 DE Platelet aggregation inhibitor, Salmosin.  
 XX  
 KW Salmosin; inhibit; blood; platelet aggregation; venom; Korean;  
 KW salmosa viper; Agkistrodon halys brevicaudus; treatment; thrombosis.  
 XX  
 OS Gloydinus halys brevicaudus.  
 XX  
 PN FR2736266-A1.  
 XX  
 PD 10-JAN-1997.  
 XX

PF	24-AUG-1995;	95FR-00010049.
PR	05-JUL-1995;	95KR-00019685.
PA	(MOGA-)	MOGAM BIOTECHNOLOGY RES INST.
XX		
XX		
P1	In CK, Kwang HC, Soo JL, Doo SK, Hak DK, Yung DY, Jeong HY,	
DR	Hong MW,	
XX		
XX	WPI: 1997-121376/12.	
PT		
PT	Peptide derived from Korean salmosa viper venom - useful as blood	
XX	platelet aggregation inhibitor, for the management of thrombosis.	
XX		
PS	Claim 1, Page 11, 15pp; French.	
XX		
CC	This peptide, designated Salmosin, inhibits blood platelet aggregation.	
CC	It is derived from the venom of the Korean salmosa viper (Agkistrodon	
CC	halys brevicaudus). Salmosin can be used, in particular, in compositions	
CC	for management of thrombosis. Salmosin also has higher activity than	
CC	kitrin, gamma-crigranin and echistatin. (Updated on 17-OCT-2003 to	
CC	standardise OS field)	
XX		
50	Sequence 73 AA;	

Query Match	90.6%;	Score 346;	DB 2;	Length 73;
Best Local Similarity	87.5%;	Pred. No. 9.4e-27;		
Matches	56;	Conservative	5;	Mismatches 3;
			Indels	0;
			Gaps	0;
Qy	2	AAPAPCCDAATCTCTTSSGACAGLCCDDCKEMKECTGTCRRARGDLDIDYCNGISAGCPBN	61	
	:			
Db	10	SPGAPCCDAATCTCTKRGAGACAGLCCDDCKRFMEKSTICRRARGDLDIDYCNGISAGCPBN	69	
	:			
Qy	62	PFHA	65	
	:			
b	70	PFHA	73	

ID	AAV58231 standard; protein; 73 AA.	RESULT 4
XX	AAV58231	AAV58231
AC	AAV58231;	
XX		
DT	12-SEP-2003 (revised)	
DT	27-MAR-2000 (first entry)	
XX		
DE	Korean snake venom salmosin.	
KM	Salmosin; angiogenesis; inhibitor; integrin; antagonist; disintegrin;	
XX	metastasis; cancer; tumour.	
OS	Glycydus halys.	
XX		
FH	Key	location/Qualifiers
FT	Region	51..53
FT		/note="RGD motif"
XX		
PN	EP967276-A2.	
XX		
PD	29-DEC-1999.	
XX		
PF	23-JUN-1999; 99EP-00304935.	
XX		
PR	23-JUN-1998; 98KR-00023778.	
XX	04-JUN-1999; 99KR-00020579.	
PA	(KIMD/) KIM D.	
XX		
PI	Kim D, Chung KH, Kang I;	
DR	WPI; 2000-064611/06.	
DR	N-PSDB; AA255609.	

XX Novel polypeptides used for antitumor therapy.  
PT  
XX  
PS Claim 1; Page 13; 24pp; English.

CC This sequence represents a 7.5 kD salmosin protein of a Korean snake,  
CC Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a family of  
CC small proteins mainly derived from snake venom which contain an RGD or  
CC KGD motif (the structural motif recognised by platelet fibrinogen  
CC receptor alpha-2-beta-3). Disintegrins act as potent antagonists of  
CC several integrins including alpha-v-beta-3 and alpha-5-beta-1 integrins,  
CC the former being a marker of angiogenic blood vessels and certain  
CC malignant cells. Disintegrins inhibit tumour metastasis by blocking  
CC tumour cell adhesion to the extracellular matrix, and antagonism of  
CC integrin alpha-v-beta-3 can suppress tumour-induced angiogenesis.  
CC Salmosin can be used as an anticancer agent. It may be used for the  
CC inhibition or reduction of tumour cell angiogenesis, the inhibition of  
CC metastatic tumour formation and the inhibition or reduction of metastatic  
CC tumour growth. Nucleotides encoding salmosin may be used in gene therapy  
CC applications. Many types of cancer may be treated with salmosin or  
CC nucleotides encoding it, including leukemia and cancers of the breast,  
CC ovary, uterus, skin, lung, larynx colon, pancreas, testis, liver, brain,  
CC muscle and bone. (Updated on 12-Sep-2003 to standardise OS field)

[illegible]

PT	New cDNA encoding Saxatillin protein derived from venom of Korean snake
AG	Agrakistron saxatillis emelianov, useful as anti-platelet aggregation
agent	and anti-tumor agent.
XX	
DR	WPI; 2002-241903/29.
Pt	Hong S., Koh Y., Sohn Y., You W., Jang Y., Huh C;
XX	
PA	(CHUN/) CHUNG K.
XX	(KIMD/) KIM D.
PR	26-JUL-2000; 2000WO-KR000809.
XX	
PF	26-JUL-2000; 2000WO-KR000809.
PD	21-FEB-2002.
PN	WO200214488-A1.
OS	Glyodius halys brevicaudus.
DE	Agrakistron halys brevicaudus salmosin protein.
KM	Korean snake; saxatillin; anticoagulant; cytostatic; venom; anti-tumour,
platelet	aggregation; anglogenesis; salmosin; cytotoxicity.
DT	18-JUN-2002 (first entry)
XX	
DT	29-AUG-2003 (revised)
AC	AAE19791;
ID	AAE19791 standard; protein; 73 AA.
RESULT	5



SQ Sequence 73 AA;

Query Match 88.2%; Score 337; DB 2; Length 73;  
 Best Local Similarity 87.3%; Pred. No. 7.2e-26;  
 Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRRAGDDLDYCNGISAGCPN 61  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 11 SPENPCDDAATCKLRGAGCAGDLCCDCKFMKEGTVCRRAGDDVDYCNGISAGCPN 70  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 62 PFH 64  
 :|||  
 DB 71 PFH 73  
 :|||

RESULT 8

AAR06395  
 ID AAR06395 standard; protein; 73 AA.

AC AAR06395;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 13-DEC-1990 (first entry)  
 XX  
 DE Albolabrin.  
 XX  
 KM Fibrinogen binding; inhibitor; platelet aggregation; thrombosis;  
 KM Viper venom.  
 XX  
 OS Trimeresurus albolabris.  
 XX  
 PN EP382451-A.  
 XX  
 PD 16-AUG-1990.  
 XX  
 PF 05-FEB-1990; 90EP-00301181.  
 XX  
 PR 07-FEB-1989; 89US-00307642.  
 XX  
 PA (MERCK & CO INC.  
 PA (UTEM) UNITV TEMPLE.  
 PA (FRIE/) FRIEDMAN P A.  
 XX  
 PI Friedman PA, Jacobs JW, Gould RJ, Polokoff MA, Gan ZR;  
 PI Niewiarowski S, Holt JC, Rucinaki B;  
 XX  
 DR WPI; 1990-248351/33.  
 XX  
 PT Viper venom polypeptide(s) - useful for inhibiting fibrinogen binding to  
 PT human platelets and inhibiting fibrinogen-induced aggregation.  
 XX  
 PS Claim 2; Page 13; 13pp; English.  
 XX  
 CC The peptide is prepd. from the venom of the viper T. albolabris or may be  
 CC prepd. by genetic engineering or solid phase synthesis. It inhibits both  
 CC fibrin binding to human platelets and fibrinogen-induced aggregation of  
 CC human platelets. It is eliminated from the circulation rapidly and is  
 CC therefore useful in situations where a strong antithrombotic action of  
 CC short duration is needed, e.g. in surgery on peripheral arteries, in  
 CC cardiovascular surgery and the interaction of platelets with artificial  
 CC surfaces. See also AAR06389-97. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 CC  
 XX  
 SQ Sequence 73 AA;

Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRRAGDDLDYCNGISAGCPN 61  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 10 SPANPCDDAATCKLRGAGCAGDLCCDCKFMKEGTVCRRAGDDLDYCNGISAGCPN 69  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 PFH 65  
 :|||  
 DB 70 PLHA 73  
 :|||

RESULT 9

AAR10106  
 ID AAR10106 standard; protein; 73 AA.

XX AAR10106;  
 AC  
 XX  
 DT 13-MAR-1991 (first entry)  
 XX  
 DE Trigramin-gamma.  
 XX  
 KM Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition;  
 KM GP IIA; GP IIA; hypercoagulation.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9015072-A.  
 XX  
 PD 13-DEC-1990.  
 XX  
 PF 07-JUN-1989; 89US-00362718.  
 XX  
 PR 07-JUN-1989; 89US-00362718.  
 XX  
 PA (GETH) GENENTECH INC.  
 PA  
 PI Lazarus R, Dennis M;  
 PI  
 DR WPI; 1991-007159/01.  
 DR N-PSDB; AAQ10160.  
 XX  
 PT Platelet aggregation inhibiting amino acid sequences - are derived from  
 PT snake venom and inhibit fibrinogen binding to GP IIA-GP IIA.  
 XX  
 PS Disclosure; Fig 1; 91pp; English.  
 XX  
 CC The sequence was produced by recombinant techniques using a synthetic  
 CC gene prepd. from 10 oligonucleotides based on the amino acid sequence  
 CC determined by Edman degradation. The recombinant trigramin-gamma is used  
 CC in treatment of hypercoagulation-related states. See also AAR10107-R10113  
 CC  
 XX  
 SQ Sequence 73 AA;

Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRRAGDDLDYCNGISAGCPN 61  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 DB 10 SPANPCDDAATCKLRGAGCAGDLCCDCKFMKEGTVCRRAGDDLDYCNGISAGCPN 69  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 QY 62 PFH 65  
 :|||  
 DB 70 PLHA 73  
 :|||

RESULT 10  
 AAR53946  
 ID AAR53946 standard; peptide; 73 AA.

XX AAR53946;  
 AC  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Disintegrin peptide #14.  
 XX  
 KM Disintegrin; Viperidae; snake; integrin; inhibitor; fibrinogen;

KW integrin binding sites; GP IIb/IIIa; human; platelets; radiolabel;  
 KW treatment; diagnosis; venous; arterial; thrombi; pulmonary emboli;  
 KW tumours; abscesses; thrombus component.  
 XX  
 OS Trimeresurus albolabris.  
 XX  
 PN WO9409036-A1.  
 XX  
 PD 28-APR-1994.  
 XX  
 PF 05-OCT-1993; 93WO-US009523.  
 XX  
 PR 19-OCT-1992; 92US-00965674.  
 XX  
 PA (UTEM) UNIV TEMPLE.  
 XX  
 PI Knight LC, Maurer AH;  
 XX  
 DR WPI; 1994-151248/18.  
 XX  
 PT Radio-labelled polypeptide(s) derived from Viperidae disintegrin(s) - for  
 PT treatment and diagnosis of venous and arterial thrombi, pulmonary emboli  
 PT and tumours or abscesses having a thrombus component.  
 XX  
 PS Claim 28; Page 48; 62pp; English.  
 XX  
 CC The sequences given in AAR53933-46 are disintegrin peptides. Disintegrins  
 CC are low molecular weight proteins from the Viperidae family of snakes  
 CC which bind integrin proteins similar to the endogenous messenger and  
 CC structurally interactive molecules. Disintegrins are competitive  
 CC inhibitors of biomolecules, such as fibrinogen, for integrin binding  
 CC sites such as GP IIb/IIIa on human platelets. Disintegrins contain the  
 CC tripeptide sequence Arg-Gly-Asp. Radiolabelled disintegrin peptides can  
 CC be used for the treatment and diagnosis of venous and arterial thrombi.  
 CC pulmonary emboli and tumours or abscesses that have a thrombus component.  
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to  
 CC correct OS field.)  
 XX  
 SQ Sequence 73 AA;  
 XX  
 Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 OY 2 APANPCDAATCKLTGSGCADGLCCDQCKFMKEGTGCRARAGDDLDYCNGISAGCPRN 61  
 DB 10 SPANPCDAATCKLPGAGCGRGLCCDQCKFMKEGTICRRAGDDLDYCNGISAGCPRN 69  
 OY 62 PFHA 65  
 DB 70 PLHA 73  
 XX  
 RESULT 11  
 AAW45500  
 ID AAW45500 standard; peptide; 73 AA.  
 XX  
 AC AAW45500;  
 XX  
 DT 20-MAY-1998 (first entry)  
 XX  
 DE Albolabrin peptide targeting ligand.  
 XX  
 DE Contrast agent; targeted composition; diagnosis; diseased tissue;  
 KW glycoprotein GPIIb/IIIa receptor; albolabrin.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9640285-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US009938.

XX  
 PR 07-JUN-1995; 95US-00497684.  
 PR 01-MAY-1996; 96US-00640464.  
 XX  
 PA (IMAR) IMARX PHARM CORP.  
 XX  
 PI Unger EC, Shen D, Wu G;  
 XX  
 DR WPI; 1997-077233/07.  
 XX  
 PT Contrast agent or targeted compsn. for imaging or treating diseased  
 PT tissue - comprising lipid, protein or polymer, a gas, and a targeting  
 PT ligand e.g. a protein, peptide, saccharide or steroid.  
 XX  
 PS Disclosure; Page 57; 175pp; English.  
 XX  
 CC This sequence represents a targeting ligand. The invention relates to a  
 CC contrast agent for diagnostic imaging or a target composition which  
 CC comprises: (i) a lipid, protein or polymer and (ii) a gas, in combination  
 CC with (iii) a targeting ligand (TL). TL targets cells or receptors  
 CC selected from myocardial, endothelial, epithelial and tumour cells and  
 CC the glycoprotein GPIIb/IIIa receptor. Also claimed are: a composition  
 CC comprising vesicles containing (i) - (iii) and an aqueous carrier; a  
 CC targeted vesicle composition comprising a fluorinated gas and a targeting  
 CC ligand (TL) which targets tissues or receptors; a formulation for  
 CC therapeutic or diagnostic use comprising (i)-(iii) and a bioactive agent;  
 CC and a method for providing an image of an internal region of a patient,  
 CC or for diagnosing the presence of diseased tissue, comprising: (a)  
 CC administration of a composition as above; and (b) scanning the patient  
 CC using ultrasound to obtain a visible image of the region or diseased  
 CC tissue. The methods and compounds are useful for imaging or diagnosing  
 CC the presence of diseased tissue, especially myocardial, endothelial or  
 CC epithelial tissue but also gastrointestinal and cardiovascular regions.  
 CC In particular the ligand targets regions of arteriosclerosis. Stabilised  
 CC vesicles are particularly useful for perfusion imaging. The vesicles may  
 CC also be used to deliver active agents to an intended target such as  
 CC tissue or a receptor, and ultrasound can then be used to promote rupture  
 CC of the vesicles and release a bioactive or diagnostic agent  
 XX  
 SQ Sequence 73 AA;  
 XX  
 Query Match 87.4%; Score 334; DB 2; Length 73;  
 Best Local Similarity 84.4%; Pred. No. 1.4e-25;  
 Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 OY 2 APANPCDAATCKLTGSGCADGLCCDQCKFMKEGTGCRARAGDDLDYCNGISAGCPRN 61  
 DB 10 SPANPCDAATCKLPGAGCGRGLCCDQCKFMKEGTICRRAGDDLDYCNGISAGCPRN 69  
 OY 62 PFHA 65  
 DB 70 PLHA 73  
 XX  
 RESULT 12  
 ADH67966  
 ID ADH67966 standard; peptide; 73 AA.  
 XX  
 AC ADH67966;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Composition targeting ligand peptide Albolabrin.  
 XX  
 DE bioactive agent; anionic lipid; cationic counter ion;  
 KW lipid covalently bonded to a polymer; ultrasound; charged lipid;  
 KW targeted drug delivery; diagnostic imaging; targeting ligand;  
 KW GPIIb/IIIa receptor; diagnosis; vascular thrombosis; clot.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9842383-A1.

[illegible]

PD	10-AUG-2000.
XX	
XX	02-FEB-2000; 2000WO-US002620.
XX	
PR	03-FEB-1999; 99US-00243640.
XX	
PA	(IMAR-) IMARX PHARM CORP.
XX	
XX	Unger EC, Wu Y;
XX	
DR	WPI; 2000-532867/48.
XX	
PT	Ultrasound method, useful for diagnosis of e.g. thrombi or carcinomas,
PT	uses different types of energy for printing and interrogating the subject.
PS	Disclosure; Page 70; 211p; English.
XX	
CC	The present invention describes an ultrasound method comprising: (1)
CC	administering a targeted vesicle composition (A); and (ii) scanning the
CC	subject by exposure to a first type of ultrasound energy and then
CC	interrogating with a second type of ultrasound energy. (A) consists of a
CC	vesicle comprising a lipid, protein or polymer, encapsulating a gas, in
CC	combination with a targeting ligand. The method is used to detect: (i) a
CC	thrombus (particularly old or echogenic); (ii) a low concentration of
CC	vesicles; or (iii) vesicles targeted to endothelial tissue, particularly
CC	those containing integrins associated with malignancy or inflammation in
CC	early or small lesions, e.g. atherosclerotic plaque or ovarian.
CC	endothelial or other carcinomas. The method increases the signal from
CC	microbubbles and reduces background noise. The present sequence
CC	represents a targeting ligand peptide which is used in the method of the
CC	present invention
XX	
SO	Sequence 73 AA;
XX	
Query Match	87.4%; Score 334; DB 3; Length 73;
Best Local Similarity	84.4%; Pred. No. 1,4e-25;
Matches 54; Conservative	5; Mismatches 5; Indels 0; Gaps 0;
OY	2 APANPCDAAATCKLTGSCADGHCDCQCKFMKEGTVCRPARGDDLDYCNGISAGCPRN 61
DB	10 SPANPCDAAATCKLTPAQCGEGCLCCQCSFPMKGTTCRRARGBDDLDYCNGISAGCPRN 69
OY	62 PFPA 65
DB	70 PLPA 73
XX	
RESULT 14	
ABG30392	
ID	ABG30392 standard; protein; 73 AA.
XX	
AC	ABG30392;
XX	
DT	07-OCT-2002 (first entry)
XX	
DE	Glycoprotein GpIbIIa targeting ligand Albolabrin.
XX	
KM	Target vesicle; diagnostic imaging; thrombus; cancer; albolabrin;
KM	arteriosclerosis; atherosclerotic plaque; infarcted myocardium;
KM	glycoprotein GpIbIIa receptor; targeting ligand.
OS	Unidentified.
XX	
PN	WO200236161-A2.
XX	
PD	10-MAY-2002.
XX	
PF	17-OCT-2001; 2001WO-US032308.
XX	
PR	30-OCT-2000; 2000US-0069679.
XX	
PA	(IMAR-) IMARX THERAPEUTICS INC.
XX	





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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:12:57 ; Search time 39 Seconds  
(without alignments)  
160.361 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483

Perfect score: 382

Sequence: 1 DAPANPCDAATCKLTGSGQ.....DDDYCNGISAGCPNPFHA 65

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	90.6	71	2	AS9409
2	336	88.0	484	2	JC8020
3	334	87.4	73	2	A23731
4	334	87.4	73	2	E35982
5	333	87.2	71	2	A59411
6	333	87.2	73	2	A59410
7	326	85.3	73	2	D35982
8	322	84.3	480	1	A30065
9	321.5	84.2	71	2	A33990
10	286	74.9	71	2	G43019
11	286	74.9	72	2	I43019
12	285	74.6	73	2	H43019
13	282	73.8	72	2	B43020
14	276	72.3	73	2	B43019
15	272	71.2	73	2	B40003
16	270	70.7	73	2	A43020
17	269	70.4	72	2	F43019
18	269	70.4	72	2	B43019
19	269	70.4	72	2	D43019
20	268	70.2	73	2	C43019
21	266	69.6	73	2	A43019
22	264	69.1	73	2	A40003
23	263	68.8	71	2	A59412
24	261	68.3	481	2	A59413
25	260	68.1	71	2	A59413
26	257	67.3	71	2	S13168
27	251	65.7	481	2	JC4342
28	248	64.9	70	2	A58649
29	241	63.1	75	2	JX0169

30	236	61.8	478	2	JQ1301	hemorrhagic protei
31	235	61.5	478	2	JC4880	fibrinolytic metal
32	228	59.7	478	2	A43295	atrolysin E (BC 3.
33	223.5	58.5	83	2	F35982	bican alpha - puff
34	221.5	58.0	83	2	A4156	biticatin - puff
35	214	56.0	616	2	A55796	ecarin precursor -
36	199	52.1	429	2	A42972	coagulation factor
37	196.5	51.4	617	2	S48160	metalloproteinase
38	195.5	51.2	571	2	S24789	jararagin C precu
39	193.5	51.2	609	2	S55270	caricollastatin p
40	194.5	50.9	419	2	A59414	metalloproteinase
41	194	50.8	47	2	A35982	echistatin alpha-2
42	192.5	50.4	610	2	JC7530	vaecular apoptosis
43	191	50.0	49	2	A3029	echistatin alpha-1
44	189	49.5	50	2	S53431	echistatin beta -
45	188.5	49.3	419	2	S41607	atrolysin A (BC 3.

#### ALIGNMENTS

##### RESULT 1

AS9409  
platelet-aggregation disintegrin (brevicaudin) 2b, venom - Glycydus halys brevicaudus  
C:Species: Glycydus halys brevicaudus  
C:Date: 01-Mar-2002 #sequence\_revision 01-Mar-2002 #text\_change 09-Jul-2004  
C:Accession: AS9409

R:Iterada, S.

Fukuoka Univ. Sci. Reports 30, 71-78, 2000

A:Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Glycyd.

A:Reference number: AS9409

A:Accession: AS9409

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-71 <TER>

A:Cross-references: UNIPROT:Q90WC0

C:Keywords: anticoagulant; integrin inhibitor; venom

Query Match 90.6%; Score 346; DB 2; Length 71;

Best Local Similarity 87.5%; Pred. No. 3.2e-27;

Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APANPCDAATCKLTGSGQADGLCCDCKFKKEGTGCRARGDLDYCNGISAGCPN 61

DB 8 SGNPCDAATCKLRQGNQCAEGLCCDCKFRKEGTICRRARGDLDYCNGISAGCPN 67

QY 62 PFHA 65

DB 68 PFHA 71

##### RESULT 2

JC8020

metalloproteinase-disintegrin protein, Jerdonitlin - Trimeresurus jerdonitli

C:Species: Trimeresurus jerdonitli

C:Date: 04-Apr-2004 #sequence\_revision 04-Apr-2004 #text\_change 04-Apr-2004

C:Accession: JC8020; PC7231

R:Chen, K.Q.; Jin, Y.; Wu, J.B.; Zhou, X.D.; Lu, Q.M.; Wang, W.Y.; Xiong, Y.L.

Biochem. Biophys. Res. Commun. 310, 182-187, 2003

A:Title: A new protein structure of P-II class snake venom metalloproteinases: It compr

A:Reference number: JC8020; PMID: 14511668

A:Accession: JC8020

A:Molecule type: mRNA

A:Residues: 1-484 <CHE>

A:Cross-references: GB:AY364231

A:Experimental source: Crude venom

A:Accession: PC7231

A:Molecule type: protein

A:Residues: 206-214;221-233;299-308;310-344;451-453;460-484 <CH2>

C:Comment: This protein, a new metalloproteinase-disintegrin protein, belongs to the cla

action with IC50 of 120nM.

C:Keywords: Jerdonitlin; metalloproteinase-disintegrin; platelet aggregation; SWP

```

Query Match 51: 98.0%; Score 336; DB 2; Length 484;
Best Local Similarity 90.2%; Pred. No. 1.2e-25;
Matches 55; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 5 NPCCDAATCKLTGSGCADGLCCDQCKEMKEGTVCRARAGDLDLYCNGISAGCPNPFH 64
Db NPCCDAATCKLTGSGCADGLCCDQCKEMKEGTVCRARAGDLDLYCNGISAGCPNPFH 483
65 A 65
|
484 A 484

RESULT 3
A23731
albolabrin - green pit viper
C:Species: Trimeresurus albolabris (green pit viper)
C:Date: 28-Feb-1992 #sequence_revision 23-Aug-1997 #text_change 09-Jul-2004
C:Accession: A23731; S43021
R:Calveire, J.J.; Schaefer, W.; Soszka, T.; Lu, W.; Cook, J.J.; Jameson, B.A.; Niewiarowski
Biochemistry 30, 5225-5229, 1991
A:Title: Identification of the disulfide bond pattern in albolabrin, an RGD-containing
story activity
A:Reference number: A23731; MUID:91242430; PMID:2036389
A:Accession: A23731
A:Molecule type: protein
A:Residues: 1-73 <CAL>
A:Cross-references: UNIPROT:P17496
R:Jalaja, M.; Smith, K.J.; Lu, X.; Williams, J.A.; Trayer, H.; Trayer, I.P.; Hyde, E.I.
Eur. J. Biochem. 218, 853-860, 1993
A:Title: (1)H-NMR studies and secondary structure of the RGD-containing snake toxin, albolabrin
A:Reference number: S43021; MUID:94109384; PMID:8281937
A:Accession: S43021
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-73 <JAS>
C:Function:
A:Description: inhibits cell adhesion and platelet aggregation
C:Superfamily: unassigned disintegrins; disintegrin homology
C:Keywords: venom
F:1-69/Domain: disintegrin homology (Fragment) <DIS>
F:51-53/Region: cell attachment (R-G-D) motif
F:29-59,47-66/Disulfide bonds: #status experimental

Query Match 87.4%; Score 334; DB 2; Length 73;
Best Local Similarity 84.4%; Pred. No. 4.8e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 2 APANCCAAATCKLTGSGCADGLCCDQCKEMKEGTVCRARAGDLDLYCNGISAGCPN 61
Db APANCCAAATCKLTGSGCADGLCCDQCKEMKEGTVCRARAGDLDLYCNGISAGCPN 69
10 SPANPCAAATCKLTGSGCADGLCCDQCKEMKEGTVCRARAGDLDLYCNGISAGCPN 69
62 PFHA 65
|
70 PLHA 73

RESULT 4
E35982
trigramin gamma - Indian green tree viper
C:Species: Trimeresurus gramineus (Indian green tree viper)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Aug-2004
C:Accession: E35982
R:Dennis, M.S.; Henzel, W.J.; Pitti, R.M.; Lipari, M.T.; Napier, M.A.; Delsher, T.A.; Boudreau, N.;
Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990
A:Title: Platelet glycoprotein IIb/IIIa protein antagonists from snake venoms: evidence
A:Reference number: A35982; MUID:90207217; PMID:2320569
A:Accession: E35982
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-73 <DEN>
A:Cross-references: UNIPROT:P17496
C:Superfamily: disintegrin homology

```

F:1-69/pomatin disintegrin homology (fragment) <DIS>									
F:51-53/Region: cell attachment (R-G-D) motif									
Query Match 87.4%; Score 334; DB 2; Length 73;									
Best Local Similarity 84.4%; Pred. No. 4.0e-26;									
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;									
Oy	2	APANPCDDATCKLTTSQCADGLCCDQCKFMKEGTVCRPARGDDDDYCNGISAGCPRN	61						
Db	10	SPANPCDDATCKLLPQAGCEGLCCDQCKFMKKGTVCRPARGDDDDYCNGISAGCPRN	69						
Oy	62	PFHA	65						
Db	70	PLHA	73						
RESULT 5									
A:Accession: A59411									
platelet-aggregation disintegrin (brevicaudin) 1a - Gloydus halys brevicandus									
C:Species: Gloydus halys brevicandus									
C:Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004									
C:Accession: A59411									
R:Terada, S.									
Fukuoka Univ. Sci. Reports 30, 71-78, 2000									
A:Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloydus									
A:Accession: A59411									
A:Status: preliminary									
A:Molecule type: protein									
A:Residues: 1-71 <TER>									
A:Cross-references: UNIPROT:Q90220									
C:Keywords: anticoagulant; integrin inhibitor; venom									
Query Match 87.2%; Score 333; DB 2; Length 71;									
Best Local Similarity 84.4%; Pred. No. 5.9e-26;									
Matches 54; Conservative 6; Mismatches 4; Indels 0; Gaps 0;									
Oy	2	APANPCDDATCKLTTSQCADGLCCDQCKFMKEGTVCRPARGDDDDYCNGISAGCPRN	61						
Db	8	SPGNPCDDATCKLRGAGCAGELCCDQCKFMKKGTVCRIRAGDDDDYCNGISAGCPRN	67						
Oy	62	PFHA	65						
Db	68	PFHA	71						
RESULT 6									
A:Accession: A59410									
platelet aggregation disintegrin (brevicaudin) 1b, venom - Gloydus halys brevicandus									
C:Species: Gloydus halys brevicandus									
C:Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004									
C:Accession: A59410									
R:Terada, S.									
Fukuoka Univ. Sci. Reports 30, 71-78, 2000									
A:Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloydus									
A:Reference number: A59409									
A:Accession: A59410									
A:Status: preliminary									
A:Molecule type: protein									
A:Residues: 1-73 <TER>									
A:Cross-references: UNIPROT:Q90220									
C:Keywords: anticoagulant; integrin inhibitor; venom									
Query Match 87.2%; Score 333; DB 2; Length 73;									
Best Local Similarity 84.4%; Pred. No. 6e-26;									
Matches 54; Conservative 6; Mismatches 4; Indels 0; Gaps 0;									
Oy	2	APANPCDDATCKLTTSQCADGLCCDQCKFMKEGTVCRPARGDDDDYCNGISAGCPRN	61						
Db	10	SPGNPCDDATCKLRGAGCAGELCCDQCKFMKKGTVCRIRAGDDDDYCNGISAGCPRN	69						
Oy	62	PFHA	65						

Db 70 PFHA 73

## RESULT 7

C:Species: Trimeresurus gramineus (Indian green tree viper)

C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Aug-2004

C:Accession: D35982

R:Denmis, M.S.; Henzel, W.J.; Picci, R.M.; Lipari, M.T.; Napier, M.A.; Deisher, T.A.; Bu Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990

A:Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: evidence

A:Reference number: A35982; PMID:90207217; PMID:2320569

A:Accession: D35982

A:Molecule type: protein

A:Residues: 1-73 &lt;DB&gt;

A:Cross-references: UNIPROT:P17495

A:Accession: C35982

A:Molecule type: protein

A:Residues: 1-72 &lt;DB&gt;

C:Superfamily: disintegrin homology

C:Keywords: venom

F:1-73/Product: trigramin beta-2 #status experimental &lt;MA2&gt;

F:1-72/Product: trigramin beta-1 #status experimental &lt;MA1&gt;

F:1-72/Domain: disintegrin homology (fragment) &lt;DIS&gt;

F:51-53/Region: cell attachment (R-G-D) motif

Query Match 85.3%; Score 326; DB 2; Length 73;

Best Local Similarity 82.8%; Pred. No. 2.9e-25;

Matches 53; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 62 PFHA 65

Db 70 PFHA 73

RESULT 8

A:Accession: A30065

A:Molecule type: protein

A:Residues: 408-479 &lt;HUN&gt;

R:Hung, T.F.; Holt, J.C.; Lukasiwicz, H.; Niewiarowski, S.

J. Biol. Chem. 262, 16157-16163, 1987

A:Title: Trigramin. A low molecular weight peptide inhibiting fibrinogen interaction with

A:Reference number: A29784; PMID:88058981; PMID:3680247

A:Accession: A29784

A:Molecule type: protein

A:Residues: 408-419 &lt;HUN&gt;

C:Superfamily: trigramin precursor; disintegrin homology

C:Keywords: anticoagulant; glycoprotein; hydrolase; metalloproteinase; venom; zinc; zym

F:1-18/Domain: signal sequence #status predicted &lt;SIG&gt;

F:398-476/Domain: disintegrin homology &lt;DIS&gt;

F:408-479/Product: trigramin #status experimental &lt;MAT&gt;

F:458-460/Region: cell attachment (R-G-D) motif

F:279/Binding site: carboxylate (Asn) (covalent) #status predicted

F:333,337,343/Binding site: zinc (His) #status predicted

F:334/Active site: Glu #status predicted

Query Match 84.3%; Score 322; DB 1; Length 480;

Best Local Similarity 82.8%; Pred. No. 2.8e-24;

Matches 53; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 62 PFHA 65

Db 477 PFHA 480

RESULT 9

A:Accession: A33990

A:Molecule type: protein

A:Residues: 1-71 &lt;CHA&gt;

A:Cross-references: UNIPROT:P1638

C:Superfamily: unassigned disintegrins; disintegrin homology

F:1-68/Domain: disintegrin homology (fragment) &lt;DIS&gt;

Query Match 84.2%; Score 321.5; DB 2; Length 71;

Best Local Similarity 85.7%; Pred. No. 7.8e-25;

Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Db 62 PFH 64

Db 69 PFH 71

RESULT 10

A:Accession: G43019

A:Molecule type: protein

A:Residues: 1-71 &lt;SCA&gt;

A:Cross-references: UNIPROT:P1987

C:Superfamily: disintegrin homology

F:2-68/Domain: disintegrin homology &lt;DIS&gt;

Query Match 74.9%; Score 286; DB 2; Length 71;

Best Local Similarity 74.6%; Pred. No. 2.3e-21;

Matches 47; Conservative 7; Mismatches 9; Indels 0; Gaps 0;



A;Molecule type: protein  
 A;Residues: 1-73 <SCA>  
 A;Cross-references: UNIPROT:P22828  
 C;Superfamily: unassigned disintegrins; disintegrin homology  
 F;3-69/Domain: disintegrin homology <DIS>

Query Match 71.2%; Score 272; DB 2; Length 73;  
 Best Local Similarity 78.3%; Pred. No. 5.4e-20;  
 Matches 47; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 2 APANPCDDATCKLTGSGCADGLCCDQCKEMKEGTYCRARGDDLDYCNGISAGCPRN 61  
 :|||||  
 Db 10 SPANPCDDATCKLRPGACADGLCCDQCKRMRKGTVCRVARGDWNDDTCTGQADCPRN 69  
 :|||||

Search completed: November 3, 2005, 08:19:35  
 Job time : 40 secs

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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:10:02 / Search time 177 Seconds  
(Without alignments)  
188.052 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483  
Perfect score: 382  
Sequence: 1 DAPANPCCDATCKLTTSQ.....DLDDYCNIGISAGCPNPFHA 65

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	483	1	DISB_AGKCO
2	382	100.0	483	1	DISB_AGKCO
3	364	95.3	483	1	DISB_AGKPI
4	346	90.6	105	2	Q78CF2
5	346	90.6	317	2	Q90WC0
6	345	90.3	73	2	Q9DGH6
7	345	90.3	117	2	Q90221
8	345	90.3	482	2	Q9PVK9
9	342	89.5	505	2	Q73795
10	340	89.0	477	2	Q98SP2
11	339	88.7	73	2	Q78ZD5
12	336	88.0	478	2	Q78ZD9
13	336	88.0	77	2	Q80124
14	336	88.0	484	1	DISB_TRJUE
15	334	87.4	73	1	DISG_TRIAB
16	334	87.4	73	1	DISG_TRIAB
17	333	87.2	89	2	Q698K8
18	333	85.3	480	2	Q90220
19	336	85.3	73	1	DISB_TRIGA
20	334	84.8	481	1	DIS2_TRIEL
21	323	84.6	488	2	Q8AWX7
22	322	84.3	480	1	DISA_TRIGA
23	321.5	84.0	71	1	DISI_AGKPI
24	321	84.0	71	1	DISI_AGKHA
25	291	76.2	71	2	Q9YH68
26	291	76.2	466	2	Q91AX7
27	291	76.2	479	2	Q9PW78
28	291	76.2	479	2	Q9PW70
29	280	75.9	476	2	Q9Y119
30	287	75.1	73	2	Q78ZD6
31	287	75.1	466	2	Q91AX6

32	287	75.1	483	2	Q78ZEO	Q78ZEO glyoxydus sa
33	286	74.9	71	1	DISI_CROVV	P31987 crocalus vi
34	286	74.9	72	1	DISI_CROBA	P31981 crocalus ba
35	285	74.6	73	1	DISI_CROVM	P31984 crocalus mo
36	282	73.8	72	1	DISI_CROVE	P31985 crocalus vi
37	276	72.3	73	1	DISI_IACMU	P31990 lachesis mu
38	275	72.0	108	2	Q93516	Q93516 agkistrodon
39	273	71.5	243	2	Q93516	Q7813 bothrops ja
40	272	71.2	73	1	DISI_SISCT	P22828 bisrurus c
41	270	70.7	73	1	DISI_BOTJA	P31989 bothrops ja
42	269	70.4	72	1	DISI_BOTCO	P31988 bothrops co
43	269	70.4	72	1	DISI_CROAT	P31980 crocalus at
44	268	70.2	73	1	DISI_CROVL	P31986 crocalus vi
45	268	70.2	115	2	Q90222	Q90222 agkistrodon

## ALIGNMENTS

RESULT 1

ID	DISB_AGKCO	STANDARD;	PRT;	483 AA.
AC	Q805F6;			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Zinc metalloproteinase acostatin beta precursor (EC 3.4.24.-)			
DE	[contains: Disintegrin acostatin beta].			
OS	Agkistrodon contortrix contortrix (Southern copperhead).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubridae;			
OC	Viperidae; Crotalinae; Agkistrodon.			
OX	NCBI_TaxID=8713;			
RN	[1]			
RP	SEQUENCE FROM N.A., SEQUENCE OF 419-482, FUNCTION, COFACTOR, AND			
RP	SUBUNIT.			
RC	TISSUE=Venom;			
RX	PubMed=12450389; DOI=10.1021/bj025876s;			
RA	Okuda D., Koike H., Morita T.;			
RT	"A new gene structure of the disintegrin family: a subunit of dimeric			
RL	disintegrin has a short coding region.";			
RL	Biochemistry 41:14248-14254(2002).			
CC	-1- FUNCTION: The metalloproteinase is a probable venom zinc protease			
CC	that acts in hemorrhage (By similarity).			
CC	-1- FUNCTION: Acostatin inhibits fibrinogen interaction with platelet			
CC	receptors expressed on glycoprotein IIb-IIIa complex. Acts by			
CC	binding to the glycoprotein IIb-IIIa receptor on the platelet			
CC	surface and inhibits ADP-induced platelet aggregation in human			
CC	platelet-rich plasma.			
CC	-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).			
CC	-1- SUBUNIT: Acostatin is a heterodimer of an alpha and a beta			
CC	subunit.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Expressed by the venom gland.			
CC	-1- SIMILARITY: Belongs to the peptidase M12B family.			
CC	-1- SIMILARITY: Contains 1 disintegrin domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL; AB078904; BAC55945.1; -.			
DR	HSSP; P15167; 1DTH.			
DR	InterPro; IPR001762; Disintegrin.			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	InterPro; IPR001550; Peptidase_M12B.			
DR	InterPro; IPR002870; Peptidase_M12B_N.			
DR	Pfam; PF00200; Disintegrin; 1.			
DR	Pfam; PF01562; Pep_M12B_propep; 1.			

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DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN, 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS50142; ZINC PROTEASE; 1.
KW Blood coagulation; Cell adhesion; Direct protein sequencing;
KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 191
FT CHAIN 192 394
FT PROPEP 395 418
FT CHAIN 419 483
FT DOMAIN 198 394
FT DOMAIN 402 482
FT SITE 461 463
FT METAL 334 334
FT ACT SITE 335 335
FT METAL 338 338
FT METAL 344 344
FT DISULFID 369 389
FT DISULFID 349 356
FT DISULFID 425 448
FT DISULFID 426 426
FT DISULFID 431 431
FT DISULFID 439 445
FT DISULFID 444 469
FT DISULFID 457 476
SQ SEQUENCE 483 AA; 54025 MW; 6D91926570971221 CRC64;

Query Match
Best Local Similarity 100.0%; Score 382; DB 1; Length 483;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAPANPCDAATCKLTGSGCADGLCCDCKFMKEGTVCRRARGDDLDYCNIGSAGCR 60
DB 419 DAPANPCDAATCKLTGSGCADGLCCDCKFMKEGTVCRRARGDDLDYCNIGSAGCR 478
OY 61 NPFHA 65
DB 479 NPFHA 483

RESULT 2
DISI_AGKCO STANDARD; PRT; 483 AA.
ID DISI_AGKCO
AC 091AB0;
DT 05-JUL-2004 (Rel. 44, Created)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Zinc metalloprotease contortrostatin precursor (EC 3.4.24.-)
[Contains: Disintegrin contortrostatin].
OS Agkistocoda contortrix contortrix (Southern copperhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodermata; Squamata; Chordata; Serpentes; Colubroidae;
OC Viperae; Crotalinae; Agkistrodon.
OK NCBI_Taxid=8713;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 419-433, FUNCTION, COFACTOR, AND
SUBUNIT.
RC TISSUE=Venom gland;
RX MEDLINE=2016949; PubMed=10700384; DOI=10.1006/abbi.1999.1682;
RA Zhou Q., Hu P., Rittter M.R., Swenson S.D., Argounova S., Epstein A.L.,
Marland F.S.;
RT "Molecular cloning and functional expression of contortrostatin, a
homodimeric disintegrin from southern copperhead snake venom.";
RL Arch. Biochem. Biophys. 375:278-288(2000).
CC -!- FUNCTION: The metalloprotease is a probable venom zinc protease
that acts in hemorrhage (By similarity).
```

```
CC -!- FUNCTION: The disintegrin binds and inhibits integrins alpha-
CC Iib/beta-3, alpha-5/beta-1, alpha-V/beta-3, and alpha-V/beta-5. It
CC blocks cancer cell adhesion to fibronectin and vitronectin and
CC thus prevents invasion of cancer cells.
CC -!- COFACTOR: Binds 1 zinc ion per subunit.
CC -!- SUBUNIT: Homodimer; disulfide-linked (disintegrin).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the peptidase M12B family.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
-----
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-----
CC EMBL; AF212305; AAF65171.1; -.
CC HSSP; P18619; 1FVL.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN, 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS50427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS50142; ZINC PROTEASE; 1.
KW Blood coagulation; Cell adhesion; Direct protein sequencing;
KW Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 190
FT CHAIN 191 394
FT PROPEP 395 418
FT CHAIN 419 483
FT DOMAIN 198 394
FT DOMAIN 402 482
FT SITE 461 463
FT METAL 334 334
FT METAL 335 335
FT ACT SITE 338 338
FT METAL 344 344
FT METAL 344 344
FT DISULFID 369 389
FT DISULFID 349 356
FT DISULFID 425 448
FT DISULFID 439 445
FT DISULFID 444 469
FT DISULFID 457 476
SQ SEQUENCE 483 AA; 53948 MW; 2DBB370FDC590007 CRC64;

Query Match
Best Local Similarity 100.0%; Score 382; DB 1; Length 483;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAPANPCDAATCKLTGSGCADGLCCDCKFMKEGTVCRRARGDDLDYCNIGSAGCR 60
DB 419 DAPANPCDAATCKLTGSGCADGLCCDCKFMKEGTVCRRARGDDLDYCNIGSAGCR 478
OY 61 NPFHA 65
DB 479 NPFHA 483

RESULT 3
DISB_AGKPI STANDARD; PRT; 483 AA.
ID DISB_AGKPI
```



AC Q805F4; (Rel. 45, Created)  
 DT 25-OCT-2004 (Rel. 45, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Zinc metalloproteinase piscivostatin beta precursor (EC 3.4.24.-)  
 DE [containing: Disintegrin piscivostatin beta].  
 OS Agkistrodon piscivorus (Eastern cottonmouth).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Agkistrodon.  
 NC NCBI\_TaxID=8716;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SUBUNIT.  
 RC TISSUE=Venom;  
 RX PubMed=12450389; DOI=10.1021/bi025876s;  
 RA Okuda D., Koike H., Morita T.;  
 RT "A new gene structure of the disintegrin family: a subunit of dimeric  
 RT disintegrin has a short coding region.";  
 RL Biochemistry 41:14248-14254(2002).  
 RN [2]  
 RP SEQUENCE OF 415-483, AND CHARACTERIZATION OF PISCIVOSTATIN BETA.  
 RC TISSUE=Venom;  
 RX PubMed=11530017;  
 RA Okuda D., Morita T.;  
 RT "Purification and characterization of a new RGD/KGD-containing dimeric  
 RT disintegrin, piscivostatin, from the venom of Agkistrodon piscivorus  
 RT piscivorus: the unique effect of piscivostatin on platelet  
 RT aggregation.";  
 RL J. Biochem. 130:407-415(2001).  
 CC -1- FUNCTION: The metalloproteinase is a probable venom zinc protease  
 CC that acts in hemostasis (By similarity).  
 CC -1- FUNCTION: Piscivostatin inhibits fibrinogen interaction with  
 CC platelet receptors expressed on glycoprotein IIb-IIIa complex.  
 CC Acts by binding to the glycoprotein IIb-IIIa receptor on the  
 CC platelet surface and inhibits both ADP-induced platelet  
 CC aggregation and platelet aggregate dissociation in human platelet-  
 CC rich plasma.  
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).  
 CC -1- SUBUNIT: Piscivostatin is a heterodimer of an alpha and a beta  
 CC subunit.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -1- SIMILARITY: Belongs to the peptidase M12B family.  
 CC -1- SIMILARITY: Contains 1 disintegrin domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AB078906; BAC55947.1; -  
 CC HSSP: P15167; IDT.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro: IPR001590; Peptidase\_M12B.  
 DR InterPro: IPR002870; Peptidase\_M12B\_N.  
 DR Pfam: PF00200; Disintegrin; 1.  
 DR Pfam: PF01562; Pept\_M12B\_Proped; 1.  
 DR Pfam: PF01421; Reprolysin; 1.  
 DR PRINTS: PR00289; DISINTEGRIN.  
 DR ProDom: PD000664; Disintegrin; 1.  
 DR SMART: SM00050; DISIN, 1.  
 DR PROSITE: PS50215; ADAM\_MEPRO, 1.  
 DR PROSITE: PS00427; DISINTEGRIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Blood coagulation; Cell adhesion; Direct protein sequencing;  
 KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.  
 FT SIGNAL 1 20 Potential.  
 FT PROPEP 21 191 Potential.

FT CHAIN 192 394 Zinc metalloproteinase piscivostatin  
 FT PROPEP 395 414 Spacer peptide (Potential).  
 FT CHAIN 415 483 Disintegrin piscivostatin beta.  
 FT DOMAIN 198 394 Metalloprotease.  
 FT SITE 402 482 Disintegrin-like.  
 FT METAL 461 463 Cell attachment site (atypical).  
 FT METAL 334 334 Zinc (catalytic).  
 FT ACT SITE 335 335 Zinc (catalytic).  
 FT METAL 338 338 Zinc (catalytic).  
 FT METAL 344 344 Zinc (catalytic).  
 FT DISULFID 309 389 By similarity.  
 FT DISULFID 349 356 By similarity.  
 FT DISULFID 425 448 By similarity.  
 FT DISULFID 426 426 Interchain (with C-54 in alpha subunit)  
 FT DISULFID 431 431 (By similarity).  
 FT DISULFID 439 445 Interchain (with C-59 in alpha subunit)  
 FT DISULFID 444 469 (By similarity).  
 FT DISULFID 457 476 By similarity.  
 SQ SEQUENCE 483 AA; 54072 MW; FIDA9CE0F0DB3B7 CRC64;  
 Query Match 95.3%; Score 364; DB 1; Length 483;  
 Best Local Similarity 93.8%; Pred. No. 4.7e-31;  
 Matches 61; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 DAPANPCCAATCKLTTSQCADGLCCDCKFMKECTGRRARGDLDLYCNISAGCPR 60  
 DB 419 DAPANPCCAATCKLTTSQCADGLCCDCKFMKECTGRRARGDLDLYCNISAGCPR 478  
 QY 61 NPFA 65  
 DB 479 NPFA 483  
 RESULT 4  
 ID 078CP2 PRELIMINARY; PRT; 105 AA.  
 AC 078CP2;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Platelet aggregation inhibitor disintegrin (Fragment).  
 GN Name=slimosin;  
 OS Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys  
 OS brevicaudus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydius.  
 NC NCBI\_TaxID=259325;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kang I.C., Chung K.H., Lee S.J., Yun Y.D., Moon H.M., Kim D.S.;  
 RT "Purification and molecular cloning of a platelet aggregation  
 RT inhibitor from the snake (Agkistrodon halys brevicaudus) venom.";  
 RL Thromb. Res. 0:0-0(1998).  
 DR EMBL: AF054626; AAC08997.1; -  
 DR GO: GO:007229; P: integrin-mediated signaling pathway; IEA.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR001590; Peptidase\_M12B.  
 DR InterPro: IPR000519; P\_trefoll.  
 DR Pfam: PF00200; Disintegrin; 1.  
 DR Pfam: PF01421; Reprolysin; 1.  
 DR PRINTS: PR00289; DISINTEGRIN.  
 DR PROSITE: PS50215; ADAM\_MEPRO, 1.  
 DR PROSITE: PS00427; DISINTEGRIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50214; DISINTEGRIN\_2; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 KW Integrin.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 105 AA; 11407 MW; 6F10AD4496D35F2 CRC64;

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Query Match      90.6%; Score 346; DB 2; Length 105;
Best Local Similarity 87.5%; Pred. No. 1.1e-29;
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCCDATATCTTGSQCADGLCCDQCFMKEGTVCRARDDDDYCNGISACCPN 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 42 SPGNPCCDATATCTLRGAQACAEGLCCDQCFMKEGTVCRARDDDDYCNGISACCPN 101
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 PFHA 65
   ||||
Db 102 PFHA 105

RESULT 5
Q90WCO PRELIMINARY; PRT; 317 AA.
AC Q90WCO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2004 (TrEMBLrel. 19, Last sequence update)
DE Metalloprotease (Fragment).
GN Name=hxl-1;
OS Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydus halys
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
NCBI_TaxId=259325;
OK NCB1
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Xilian H.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF367868; AAK73517.1; -.
DR PIR; A59409; A59409.
DR PDB; 1L3X; NMR; A=245-317.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; Disintegrin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS50427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 317 AA; 35109 MW; 9851177BCBE2202E CRC64;

Query Match      90.6%; Score 346; DB 2; Length 317;
Best Local Similarity 87.5%; Pred. No. 2.8e-29;
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCCDATATCTTGSQCADGLCCDQCFMKEGTVCRARDDDDYCNGISACCPN 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 254 SPGNPCCDATATCTLRGAQACAEGLCCDQCFMKEGTVCRARDDDDYCNGISACCPN 313
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 PFHA 65
   ||||
Db 314 PFHA 317

RESULT 6
Q9DGH6 PRELIMINARY; PRT; 73 AA.
AC Q9DGH6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Saxatillin (Fragment).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys

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OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
NCBI_TaxId=8714;
OK NCB1
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Chung K.-H., Koh Y.-S., Hong S.-Y., Kim D.-S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY005480; AAG01882.1; -.
DR HSSP; P21859; 1J2L.
DR InterPro; IPR001762; Disintegrin.
DR Pfam; PF00200; Disintegrin; 1.
DR PRINTS; PR00289; Disintegrin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
FT NON TER 1
SQ SEQUENCE 73 AA; 7726 MW; 8F0225BBD502FE7 CRC64;

Query Match      90.3%; Score 345; DB 2; Length 73;
Best Local Similarity 87.5%; Pred. No. 1e-29;
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCCDATATCTTGSQCADGLCCDQCFMKEGTVCRARDDDDYCNGISACCPN 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 APANPCCDATATCTLRGAQACAEGLCCDQCFMKEGTVCRARDDDDYCNGISACCPN 69
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 PFHA 65
   ||||
Db 70 PFHA 73

RESULT 7
Q90221 PRELIMINARY; PRT; 117 AA.
AC Q90221;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prepro-halystatin 2 (Fragment).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
NCBI_TaxId=8714;
OK NCB1
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Fujisawa Y., Kuroda S., Notoya K., Konishi H., Terashita Z.;
RT "Halystatin", a novel disintegrin from agkistrodon halys, is a potent
RT inhibitor of bone resorption and platelet aggregation.";
RL Takeda Kenkyusho Ho 53:39-56 (1994).
DR EMBL; D28871; BAA06027.1; -.
DR HSSP; P21859; 1J2L.
DR MEROPS; M12.134; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; Disintegrin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS50427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
FT NON TER 1
SQ SEQUENCE 117 AA; 12686 MW; B1F9A98056B8A07B CRC64;

Query Match      90.3%; Score 345; DB 2; Length 117;

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Best Local Similarity 87.5%; Pred. No. 1.5e-29;  
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APANPCDDATCTCTTGGSCADGLCCDQCKFMKEGTVCRARDDDDYCNGISAGCPRN 61  
DB 54 APANPCDDATCTCTLRGACAGELCCDQCKFMKEGTVCRARDDDDYCNGISAGCPRN 113  
QY 62 PFHA 65  
DB 114 PFHA 117

## RESULT 8

Q9PVK9 PRELIMINARY; PRT; 482 AA.  
AC Q9PVK9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Metalloprotease.  
GN Name-Mt-d;  
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=brevicaudus; TISSUE=Venom;  
RA MEDLINE=9337693; PubMed=10406963;  
RA Jeon O.H., Kim D.S.;  
RT "Molecular cloning and functional characterization of a snake venom metallopeptidase";  
RT Eur. J. Biochem. 263:526-533(1999).  
DR EMBL; AF051789; AAD02654.1; -.  
DR HSSP; P21859; 1J2L.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001762; Disintegrin.  
DR InterPro; IPR001590; Peptidase\_M12B.  
DR InterPro; IPR002870; Peptidase\_M12B\_N.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR001515; Ribosomal\_L32E.  
DR Pfam; PF00200; Disintegrin\_1.  
DR Pfam; PF01562; Pep\_M12B\_propep; 1.  
DR Pfam; PF01421; Repolysin\_1.  
DR PRINTS; PR00289; DISINTEGRIN.  
DR ProDom; PD000664; Disintegrin\_1.  
DR SMART; SM00050; DISIN\_1.  
DR PROSITE; PS50215; ADAM\_MERPRO; 1.  
DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE; PS00214; DISINTEGRIN\_2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Metalloprotease; Protease.  
SQ SEQUENCE 482 AA; 53409 MW; C6014BBE7BC8B15 CRC64;

Query Match 90.3%; Score 345; DB 2; Length 482;  
Best Local Similarity 87.5%; Pred. No. 5.2e-29;

Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APANPCDDATCTCTTGGSCADGLCCDQCKFMKEGTVCRARDDDDYCNGISAGCPRN 61  
DB 419 APANPCDDATCTCTLRGACAGELCCDQCKFMKEGTVCRARDDDDYCNGISAGCPRN 478

QY 62 PFHA 65  
DB 479 PFHA 482

## RESULT 9

073795 PRELIMINARY; PRT; 505 AA.  
ID 073795;  
AC 073795;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Metalloprotease.  
GN Name-Mt-b;  
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Gloydius.  
OX NCBI\_TaxID=8714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=brevicaudus; TISSUE=Venom;  
RA Jeon O.H., Kim D.S.;  
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF051788; AAD02653.1; -.  
DR HSSP; P21859; 1J2L.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR001762; Disintegrin.  
DR InterPro; IPR001590; Peptidase\_M12B.  
DR InterPro; IPR002870; Peptidase\_M12B\_N.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR001515; Ribosomal\_L32E.  
DR Pfam; PF00200; Disintegrin\_1.  
DR Pfam; PF01562; Pep\_M12B\_propep; 1.  
DR Pfam; PF01421; Repolysin\_1.  
DR PRINTS; PR00289; DISINTEGRIN.  
DR ProDom; PD000664; Disintegrin\_1.  
DR SMART; SM00050; DISIN\_1.  
DR PROSITE; PS50215; ADAM\_MERPRO; 1.  
DR PROSITE; PS00427; DISINTEGRIN\_1; 1.  
DR PROSITE; PS50214; DISINTEGRIN\_2; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Metalloprotease; Protease.  
SQ SEQUENCE 505 AA; 56336 MW; C96E99FC9C05378F CRC64;

Query Match 89.5%; Score 342; DB 2; Length 505;  
Best Local Similarity 85.9%; Pred. No. 1.1e-28;  
Matches 55; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APANPCDDATCTCTTGGSCADGLCCDQCKFMKEGTVCRARDDDDYCNGISAGCPRN 61  
DB 442 APANPCDDATCTCTLRGACAGELCCDQCKFMKEGTVCRARDDDDYCNGISAGCPRN 501

QY 62 PFHA 65  
DB 502 PFHA 505

## RESULT 10

Q98SP2 PRELIMINARY; PRT; 477 AA.

AC Q98SP2;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Bothrops scutellatus.

OS Bothrops jararaca (Jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8724;

```

RN [1]
RP SEQUENCE FROM N.A.
RA Silva C.A., Martine de Camargo A.C., de Toledo Serrano S.M.;
RL Submitted (FE8-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF345931; AAK15542.1; -.
DR HSSP: P21859; 1J2L.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0005840; C:ribosome; IEA.
DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR GO: GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Peptidase_M12B.
DR InterPro: IPR002870; Peptidase_M12B_N.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR Pfam: PF00200; Disintegrin; 1.
DR Pfam: PF01562; Pep_M12B_propep; 1.
DR Pfam: PF01421; Reprolysin; 1.
DR PRINTS: PR00289; DISINTEGRIN.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART: SM00050; DISIN; 1.
DR PROSITE: PS50215; ADAM_MEPRO; 1.
DR PROSITE: PS00427; DISINTEGRIN_1; 1.
DR PROSITE: PS00142; DISINTEGRIN_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 477 AA; 5340 MW; AC973EE767E10B3 CRC64;

```

```

Query Match 89.0%; Score 340; DB 2; Length 477;
Best Local Similarity 87.3%; Pred. No. 1,8e-28;
Matches 55; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 3 PANPCCDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARGDLDLDYCNGISAGCPR 62
DB 415 PANPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGDMDYCNGISAGCPR 474
QY 63 NFHA 65
DB 475 NFHA 477

```

```

RESULT 11
Q7SZDS PRELIMINARY; PRT; 73 AA.
AC Q7SZDS;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Disintegrin (Fragmenet).
OS Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBL_TaxID=35671;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Snake venom gland;
RA Sun D.-Y., Yang T.-S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY204245; AAP20644.1; -.
DR HSSP: P21859; 1J2L.
DR GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro: IPR001762; Disintegrin.
DR Pfam: PF00200; Disintegrin; 1.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART: SM00050; DISIN; 1.
DR PROSITE: PS00427; DISINTEGRIN_1; 1.
DR PROSITE: PS00142; DISINTEGRIN_2; 1.
KW Integrin.
FT NON_TER 1 1
SQ SEQUENCE 73 AA; 7768 MW; 615509DF966882EF CRC64;

```

```

Query Match 88.7%; Score 339; DB 2; Length 73;
Best Local Similarity 84.6%; Pred. No. 4,5e-29;
Matches 55; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 DAPANPCCDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARGDLDLDYCNGISAGCPR 60
DB 9 DAPANPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGDMDYCNGISAGCPR 68
QY 61 NFHA 65
DB 69 NFHA 73

```

```

RESULT 12
Q7SZDS PRELIMINARY; PRT; 478 AA.
AC Q7SZDS;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Metalloprotease/disintegrin ussuri.
OS Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBL_TaxID=35671;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Snake venom gland;
RA Sun D.-Y., Yang T.-S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY204245; AAP20644.1; -.
DR HSSP: P21859; 1J2L.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0005840; C:ribosome; IEA.
DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR GO: GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR GO: GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Peptidase_M12B.
DR InterPro: IPR002870; Peptidase_M12B_N.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR InterPro: IPR001515; Ribosomal_L32E.
DR Pfam: PF00200; Disintegrin; 1.
DR Pfam: PF01562; Pep_M12B_propep; 1.
DR Pfam: PF01421; Reprolysin; 1.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART: SM00050; DISIN; 1.
DR PROSITE: PS50215; ADAM_MEPRO; 1.
DR PROSITE: PS00427; DISINTEGRIN_1; 1.
DR PROSITE: PS00142; DISINTEGRIN_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Integrin.
SQ SEQUENCE 478 AA; 53443 MW; CD2FBC975F62A771 CRC64;

```

```

Query Match 88.7%; Score 339; DB 2; Length 478;
Best Local Similarity 84.6%; Pred. No. 2,3e-28;
Matches 55; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1 DAPANPCCDAATCKLTTSQCADGLCCDQCKFMKEGTVCRARGDLDLDYCNGISAGCPR 60
DB 414 DAPANPCCDAATCKLRPGAQCAEGLCCDQCKFMKEGTVCRARGDMDYCNGISAGCPR 473
QY 61 NFHA 65
DB 474 NFHA 478

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RESULT 13
Q80124 PRELIMINARY; PRT; 77 AA.
ID Q80124

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AC Q80124;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Disintegrin (Fragment).
OS Bothrops alternatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OC NCBI_TaxID=64174;
RN [1]
RP SEQUENCE FROM N.A.
RA Ramos O.H.P., Sellastre-de-Araujo H.S.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY259516; AAO75107.1; -.
DR HSSP; P21859; 1JZL.
DR GO; GO:0007229; P: integrin-mediated signaling pathway; IEA.
DR InterPro; IPR001762; Disintegrin.
DR Pfam; PF00200; Disintegrin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
KM Integrin.
FT NON TER
SQ SEQUENCE 77 AA; 8179 MW; 680501C26E7ED496 CRC64;

Query Match 88.0%; Score 336; DB 2; Length 77;
Best Local Similarity 87.3%; Pred. No. 9; 9e-29;
Matches 55; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PNPCCDAATCKLTTSQCGADGLCCDQCFMKKGTVCRRARGGDDLDYCNGISAGCPNPP 62
DB 15 PNPCCDAATCKLTTSQCGADGLCCDQCFMKKGTVCRRARGGDDLDYCNGISAGCPNPP 74

QY 63 FHA 65
DB 75 FHA 77

RESULT 14
DIST TRIUE STANDARD; PRT; 484 AA.
AC P83912;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Zinc metalloproteinase jerdonitin precursor (EC 3.4.24.-) [Contains:
DE Disintegrin jerdonitin].
OS Trimerurus jerdoniti (Jerdon's pit-viper) (Probochrops jerdoni).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Trimerurus.
OX NCBI_TaxID=135726;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 206-214; 221-233; 299-308;
RP 310-344; 451-453 AND 460-484.
RC TISSUE=Venom;
RX MEDLINE=22873278; PubMed=14511668; DOI=10.1016/j.bbrc.2003.09.009;
RA Chen R.-Q., Jin Y., Wu J.-B., Zhou X.-D., Lu Q.-M., Wang W.-Y.,
RA Xiong Y.-L.;
RT "A new protein structure of P-II class snake venom metalloproteinases:
RT it comprises metalloproteinase and disintegrin domains.";
RL Biochem. Biophys. Res. Commun. 310:182-187(2003).
CC -1- FUNCTION: The metalloproteinase is a probable venom zinc protease
CC that acts in hemorrhage (By similarity).
CC -1- FUNCTION: jerdonitin inhibits fibrinogen interaction with platelet
CC receptors expressed on glycoprotein IIb-IIIa complex. Acts by
CC binding to the glycoprotein IIb-IIIa receptor on the platelet
CC surface and inhibits aggregation induced by ADP, thrombin,
CC platelet-activating factor and collagen (By similarity).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

```

```

CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the peptidase M12B family.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY64231; AAO63966.1; -.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR Pfam; PF00200; Disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
KM Blood coagulation; Cell adhesion; Direct protein sequencing;
KM Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KM Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 191
FT CHAIN 192 392
FT PROPEP 393 410
FT CHAIN 411 484
FT SITE 462 464
FT METAL 330 330
FT ACT SITE 331 331
FT METAL 334 334
FT METAL 340 340
FT METAL 340 340
FT DISULFID 305 387
FT DISULFID 347 352
FT DISULFID 403 422
FT DISULFID 414 432
FT DISULFID 416 427
FT DISULFID 426 449
FT DISULFID 440 446
FT DISULFID 445 470
FT DISULFID 458 477
SQ SEQUENCE 484 AA; 54613 MW; 8D603BE7C0F48232 CRC64;

Query Match 88.0%; Score 336; DB 1; Length 484;
Best Local Similarity 90.2%; Pred. No. 4; 9e-28;
Matches 55; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 NPPCCDAATCKLTTSQCGADGLCCDQCFMKKGTVCRRARGGDDLDYCNGISAGCPNPP 64
DB 424 NPPCCDAATCKLTTSQCGADGLCCDQCFMKKGTVCRRARGGDDLDYCNGISAGCPNPP 483

QY 65 A 65
DB 484 A 484

RESULT 15
DIST TRIAB STANDARD; PRT; 73 AA.
AC P62384;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Disintegrin albolabrin (Platelet aggregation activation inhibitor).
OS Trimerurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Trimeresurus.  
OX NCBI\_Taxid=8765;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Venom;  
RX MEDLINE=90283463; PubMed=2191722; DOI=10.1016/0167-4838(90)90229-9;  
RA Williams J., Ruchniski B., Holt J., Niewiarowski S.;  
RT "Elegantin and albolabrin purified peptides from viper venoms:  
RT homologues with the RGDs domain of fibrinogen and von Willebrand  
RT factor.";  
RL Biochim. Biophys. Acta 1039:81-89(1990).

RN [2]  
RP DISULFIDE BONDS.

RC TISSUE=Venom;  
RX MEDLINE=91242430; PubMed=2036389;  
RA Calvete J.J., Schaefer W., Soszka T., Lu W., Cook J.J., Jameson B.A.,  
RA Niewiarowski S.;  
RT "Identification of the disulfide bond pattern in albolabrin, an RGD-  
RT containing peptide from the venom of Trimeresurus albolabris:  
RT significance for the expression of platelet aggregation inhibitory  
RT activity.";  
RL Biochemistry 30:5225-5229(1991).

RN [3]

RP STRUCTURE BY NMR.  
RX MEDLINE=94109384; PubMed=8281937;  
RA Jasela M., Smith K.J., Lu X., Williams J.A., Trayer H., Trayer I.P.,  
RA Hyde E.I.;  
RT "1H-NMR studies and secondary structure of the RGD-containing snake  
RT toxin, albolabrin.";  
RL Eur. J. Biochem. 218:853-860(1993).

RN [4]

RP STRUCTURE BY NMR.  
RX MEDLINE=97052455; PubMed=8697089;  
RA Smith K.J., Jasela M., Lu X., Williams J.A., Hyde E.I., Trayer I.P.;  
RT "Three-dimensional structure of the RGD-containing snake toxin  
RT albolabrin in solution, based on 1H NMR spectroscopy and simulated  
RT annealing calculations.";  
RL Int. J. Pept. Protein Res. 48:220-228(1996).

-1- FUNCTION: Inhibits fibrinogen interaction with platelet receptors  
expressed on glycoprotein IIb-IIIa complex. Acts by binding to the  
glycoprotein IIb-IIIa receptor on the platelet surface and  
inhibits aggregation induced by ADP, thrombin, platelet-activating  
factor and collagen.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the disintegrin family.

DR PIR, A23731; A23731.

DR HSP, P18619; IFLV.

DR InterPro; IPR001762; Disintegrin.

DR Pfam; PF00200; Disintegrin\_1.

DR PRINTS; PR00289; DISINTEGRIN.

DR ProDom; PD000664; Disintegrin\_1.

DR SMART; SM00050; DISIN\_1.

DR PROSITE; PS00427; DISINTEGRIN\_1; 1.

DR PROSITE; PS50214; DISINTEGRIN\_2; 1.

KW Blood coagulation; Cell adhesion; Direct protein sequencing; Platelet.

FT DISULFID 6 15 Probable.

FT DISULFID 8 16 Probable.

FT DISULFID 21 35 Probable.

FT DISULFID 29 59 Probable.

FT DISULFID 34 38 Probable.

FT DISULFID 47 66 Probable.

FT SITE 51 53 Cell attachment site.

FT SITE 73 AA; 7573 MW; F7E011E2F46FEF14 CRC64;

SQ SEQUENCE

Query Match 87.4%; Score 334; DB 1; Length 73;  
Best Local Similarity 84.4%; Pred. No. 1.5e-28;

Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 62 PFA 65  
DB 70 PFA 73

Search completed: November 3, 2005, 08:18:51  
Job time : 179 secs

QY 2 APANPCDAATCTLTGSCADGLCCDCKFMKEGTVCARAGDDLDYCNGISAGCPRN 61  
DB 10 SPANPCDAATCTLTGSCADGLCCDCKFMKEGTVCARAGDDLDYCNGISAGCPRN 69

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:13:22 ; Search time 42 Seconds  
(without alignments)  
115.528 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483

Perfect score: 382  
Sequence: 1 DAPANPCDDATCKLTGSG.....DLDYCNISAGCPRNPFHA 65

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUTS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*  
  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	382	100.0	483	4	US-09-460-295B-2
2	337	88.2	72	6	5182260-21
3	337	88.2	72	6	5182260-21
4	337	88.2	73	6	5182260-2
5	337	88.2	73	6	5182260-2
6	334	87.4	73	1	US-07-965-674-14
7	334	87.4	73	4	US-08-993-165-15
8	334	87.4	73	4	US-09-243-640-13
9	334	87.4	73	4	US-08-929-847-15
10	334	87.4	73	4	US-09-460-295B-9
11	334	87.4	73	4	US-09-813-484-15
12	334	87.4	73	5	PCT-US93-09523-14
13	334	86.9	73	4	US-09-776-268A-1
14	329	86.1	73	4	US-09-540-448-15
15	329	86.1	73	4	US-10-046-801-15
16	325	85.1	99	1	US-07-623-611-5
17	325	85.1	99	1	US-07-623-611-8
18	325	85.1	99	5	PCT-US91-09108-5
19	325	85.1	99	5	PCT-US91-09108-8
20	325	85.1	106	1	US-07-623-611-4
21	325	85.1	106	5	PCT-US91-09108-7
22	325	85.1	106	5	PCT-US91-09108-4
23	325	85.1	106	5	PCT-US91-09108-7
24	323.5	84.7	71	1	US-07-602-847C-24
25	322	84.3	98	1	US-07-623-611-6
26	322	84.3	98	1	US-07-623-611-9
27	322	84.3	98	5	PCT-US91-09108-6

28	322	84.3	98	5	PCT-US91-09108-9	Sequence 9, Appl1
29	322	84.3	552	4	US-09-460-295B-8	Sequence 8, Appl1
30	321.5	84.2	71	1	US-07-965-674-10	Sequence 10, Appl1
31	321.5	84.2	71	4	US-09-460-295B-7	Sequence 7, Appl1
32	321.5	84.2	71	5	PCT-US93-09523-10	Sequence 10, Appl1
33	319	83.5	72	1	US-07-623-611-1	Sequence 1, Appl1
34	319	83.5	72	5	PCT-US91-09108-1	Sequence 2, Appl1
35	319	83.5	96	1	US-07-623-611-2	Sequence 3, Appl1
36	319	83.5	96	1	US-07-623-611-3	Sequence 2, Appl1
37	319	83.5	96	5	PCT-US91-09108-2	Sequence 3, Appl1
38	319	83.5	96	5	PCT-US91-09108-3	Sequence 3, Appl1
39	318	83.2	72	1	US-07-602-847C-23	Sequence 23, Appl1
40	307.5	80.5	73	1	US-07-965-674-5	Sequence 5, Appl1
41	307.5	80.5	73	5	PCT-US93-09523-5	Sequence 5, Appl1
42	293.5	76.8	71	6	518899-17	Patent No. 518899
43	293.5	76.8	71	6	518899-17	Patent No. 518899
44	286	74.9	71	6	518899-11	Patent No. 518899
45	286	74.9	71	6	518899-11	Patent No. 518899

## ALIGNMENTS

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RESULT 1
US-09-460-295B-2
; Sequence 2, Application US/09460295B
; Patent No. 6710030
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; FILE REFERENCE: 1279-3383/09801388
; CURRENT APPLICATION NUMBER: US/09/460,295B
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1.
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Agkistrodon contortrix
; US-09-460-295B-2

Query Match      100.0%; Score 382; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.3e-30; Indels 0; Gaps 0;
Matches 65; Conservative 0; Mismatches 0;

QY      1 DAPANPCDDATCKLTGSGCAGDGLCCDQCKFMKEGTVCRPARGDDLDDYCNISAGCPR 60
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DB      419 DAPANPCDDATCKLTGSGCAGDGLCCDQCKFMKEGTVCRPARGDDLDDYCNISAGCPR 478

QY      61 NEFHA 65
      |||||
DB      479 NEFHA 483

RESULT 2
5182260-21
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION NUMBER: 303,585
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
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;SEQ ID NO:21:
; LENGTH: 72
Query Match
Best Local Similarity 88.2%; Score 337; DB 6; Length 72;
Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTTGSCADGLCCDCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 61
Db 10 SPENPCDAATCKLRPGAQCAEGLCCDCKFMKEGTVCRRARGDDVNDYCNGISAGCPRN 69

Qy 62 PFH 64
Db 70 PFH 72

RESULT 3
5182260-21
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.;JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:21:
; LENGTH: 72
5182260-21

Query Match
Best Local Similarity 88.2%; Score 337; DB 6; Length 72;
Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTTGSCADGLCCDCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 61
Db 10 SPENPCDAATCKLRPGAQCAEGLCCDCKFMKEGTVCRRARGDDVNDYCNGISAGCPRN 69

Qy 62 PFH 64
Db 70 PFH 72

RESULT 4
5182260-2
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.;JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:2:
; LENGTH:73
5182260-2

Query Match
Best Local Similarity 88.2%; Score 337; DB 6; Length 73;
Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
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Qy 2 APANPCDAATCKLTTGSCADGLCCDCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 61
Db 11 SPENPCDAATCKLRPGAQCAEGLCCDCKFMKEGTVCRRARGDDVNDYCNGISAGCPRN 70

Qy 62 PFH 64
Db 71 PFH 73

RESULT 5
5182260-2
; Patent No. 5182260
; APPLICANT: MARAGANORE, JOHN M.;JAKUBOWSKI, JOSEPH A.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
; INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
; THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,313
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 303,585
; FILING DATE: 27-JAN-1989
; APPLICATION NUMBER: 303,590
; FILING DATE: 27-JAN-1989
; SEQ ID NO:2:
; LENGTH:73
5182260-2

Query Match
Best Local Similarity 88.2%; Score 337; DB 6; Length 73;
Matches 55; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APANPCDAATCKLTTGSCADGLCCDCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 61
Db 11 SPENPCDAATCKLRPGAQCAEGLCCDCKFMKEGTVCRRARGDDVNDYCNGISAGCPRN 70

Qy 62 PFH 64
Db 71 PFH 73

RESULT 6
US-07-965-674-14
; Sequence 14, Application US/07965674
; Patent No. 5380646
; GENERAL INFORMATION:
; APPLICANT: Knight, Linda C.
; TITLE OF INVENTION: Thrombus Detection Using
; TITLE OF INVENTION: Radiolabelled Disintegrins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: wealth System Of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,674
; FILING DATE: 19921019
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```



NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-173  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5380646e  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 73 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-965-674-14

Query Match 87.4%; Score 334; DB 1; Length 73;  
Best Local Similarity 84.4%; Pred. No. 3.2e-26;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTTGSCADGCLCCDQCFMKEGTVCRARAGDDLDYCNGISAGCPN 61  
DB 10 SPANPCDDAATCKLPGAGCGEGLCCDQCSFMKGTICRRAGDDLDYCNGISAGCPN 69  
QY 62 PFHA 65  
DB 70 PLHA 73

RESULT 7  
US-08-993-165-15  
Sequence 15, Application US/08993165A  
Patent No. 6123923  
GENERAL INFORMATION:  
APPLICANT: Unger, Evan C  
TITLE OF INVENTION: Optoacoustic Contrast Agents And Methods For Their Use  
FILE REFERENCE: UNGR1224  
CURRENT APPLICATION NUMBER: US/08/993,165A  
CURRENT FILING DATE: 1997-12-18  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 73  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence  
US-08-993-165-15

Query Match 87.4%; Score 334; DB 3; Length 73;  
Best Local Similarity 84.4%; Pred. No. 3.2e-26;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTTGSCADGCLCCDQCFMKEGTVCRARAGDDLDYCNGISAGCPN 61  
DB 10 SPANPCDDAATCKLPGAGCGEGLCCDQCSFMKGTICRRAGDDLDYCNGISAGCPN 69  
QY 62 PFHA 65  
DB 70 PLHA 73

RESULT 8  
US-09-243-640-13  
Sequence 13, Application US/09243640  
Patent No. 6521211  
GENERAL INFORMATION:  
APPLICANT: Unger, Evan C  
APPLICANT: Shen, Dekang  
APPLICANT: Wu, Guanli  
TITLE OF INVENTION: No. 6521211el Methods Of Imaging And Treatment With Targeted  
FILE REFERENCE: DUP-0463  
CURRENT APPLICATION NUMBER: US/09/243,640

CURRENT FILING DATE: 1999-02-03  
PRIOR APPLICATION NUMBER: 08/660,032  
PRIOR FILING DATE: 1996-06-06  
PRIOR APPLICATION NUMBER: 08/640,464  
PRIOR FILING DATE: 1996-05-01  
PRIOR APPLICATION NUMBER: 08/497,684  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 09/218,660  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/073,913  
PRIOR FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 73  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence  
US-09-243-640-13

Query Match 87.4%; Score 334; DB 4; Length 73;  
Best Local Similarity 84.4%; Pred. No. 3.2e-26;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTTGSCADGCLCCDQCFMKEGTVCRARAGDDLDYCNGISAGCPN 61  
DB 10 SPANPCDDAATCKLPGAGCGEGLCCDQCSFMKGTICRRAGDDLDYCNGISAGCPN 69  
QY 62 PFHA 65  
DB 70 PLHA 73

RESULT 9  
US-08-929-847-15  
Sequence 15, Application US/08929847  
Patent No. 6548047  
GENERAL INFORMATION:  
APPLICANT: Unger, Evan C.  
TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions  
FILE REFERENCE: BMS0441  
CURRENT APPLICATION NUMBER: US/08/929,847  
CURRENT FILING DATE: 1997-09-15  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 73  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Completely sythetic sequence  
US-08-929-847-15

Query Match 87.4%; Score 334; DB 4; Length 73;  
Best Local Similarity 84.4%; Pred. No. 3.2e-26;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTTGSCADGCLCCDQCFMKEGTVCRARAGDDLDYCNGISAGCPN 61  
DB 10 SPANPCDDAATCKLPGAGCGEGLCCDQCSFMKGTICRRAGDDLDYCNGISAGCPN 69  
QY 62 PFHA 65  
DB 70 PLHA 73

RESULT 10  
US-09-460-295B-9  
Sequence 9, Application US/09460295B  
Patent No. 6710030  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

```

; TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338C3/09801388
; CURRENT APPLICATION NUMBER: US/09/460,295B
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Trimeresurus albolabris
; US-09-460-295B-9

Query Match      87.4%; Score 334; DB 4; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANCCDAATCKLTGSGCADGLCCDQCKFMKEGTVCRARGDDLDDYCNGISAGCPRN 61
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DB      10 SPANCCDAATCKLPGAGCGEGLCCDQCSFMKKGITCRARGDDLDDYCNGISAGCPRN 69
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QY      62 PFHA 65
      :|||
DB      70 PLHA 73

RESULT 11
US-09-813-484-15
; Sequence 15, Application US/09813484
; Patent No. 6716412
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: No. 6716412el Methods Of Ultrasound Treatment Using Gas Or Gaseou
; FILE REFERENCE: UNGR1600
; CURRENT APPLICATION NUMBER: US/09/813,484
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/929,847
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely syntehtic sequence
; US-09-813-484-15

Query Match      87.4%; Score 334; DB 4; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANCCDAATCKLTGSGCADGLCCDQCKFMKEGTVCRARGDDLDDYCNGISAGCPRN 61
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DB      10 SPANCCDAATCKLPGAGCGEGLCCDQCSFMKKGITCRARGDDLDDYCNGISAGCPRN 69
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QY      62 PFHA 65
      :|||
DB      70 PLHA 73

PCT-US93-09523-14
; Sequence 14, Application PC/TUS9309523
; GENERAL INFORMATION:
; APPLICANT: Temple University - Of The Commonwealth
; APPLICANT: System of Higher Education
; APPLICANT: Knight, Linda C. and
; APPLICANT: Maurer, Alan H.
; TITLE OF INVENTION: Thrombus Detection Using
```

```

; TITLE OF INVENTION: Radiolabelled Disintegrins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 965,674
; FILING DATE: 19 October 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-173 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: None
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; PCT-US93-09523-14

Query Match      87.4%; Score 334; DB 5; Length 73;
Best Local Similarity 84.4%; Pred. No. 3.2e-26;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANCCDAATCKLTGSGCADGLCCDQCKFMKEGTVCRARGDDLDDYCNGISAGCPRN 61
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DB      10 SPANCCDAATCKLPGAGCGEGLCCDQCSFMKKGITCRARGDDLDDYCNGISAGCPRN 69
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QY      62 PFHA 65
      :|||
DB      70 PLHA 73

RESULT 13
US-09-776-268A-1
; Sequence 1, Application US/09776268A
; Patent No. 6537551
; GENERAL INFORMATION:
; APPLICANT: KIM, DOO-Sik
; APPLICANT: CHUNG, Kwang Hoe
; APPLICANT: KANG, In-Cheol
; TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
; FILE REFERENCE: 0136/1P73-US1
; CURRENT APPLICATION NUMBER: US/09/776,268A
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: US 09/335,088
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: KR 99-20579
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: KR 98-23778
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 73
; TYPE: PRT
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ORGANISM: Agkistrodon halys brevicaudus  
US-09-776-268A-1

Query Match 86.9%; Score 329; DB 4; Length 73;  
Best Local Similarity 84.4%; Pred. No. 5.1e-26;  
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDAATCKLTGSGCADGLCCDQCFMKEGTVCRRAGDDLDDYCNGISAGCPN 61  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 10 SPANPCDAATCKLPGAGCGEGLCCDQCFMKEGTICRRAGDDLDDYCNGISAGCPN 69

QY 62 PFHA 65  
|||||  
DB 70 PLHA 73

RESULT 14  
US-09-540-448-15  
; Sequence 15, Application US/09540448  
; Patent No. 6403056  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C.  
; TITLE OF INVENTION: Charged Lipids and Uses For The Same  
; FILE REFERENCE: UNGR1592  
; CURRENT APPLICATION NUMBER: US/09/540,448  
; CURRENT FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 08/925,353  
; PRIOR FILING DATE: 1997-09-08  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence  
US-09-540-448-15

Query Match 86.1%; Score 329; DB 4; Length 73;  
Best Local Similarity 82.8%; Pred. No. 1e-25;  
Matches 53; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDAATCKLTGSGCADGLCCDQCFMKEGTVCRRAGDDLDDYCNGISAGCPN 61  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 10 SPANPCDAATCKLPGAGCGEGLCCDQCFMKEGTICRRAGDDLDDYCNGISAGCPN 69

QY 62 PFHA 65  
|||||  
DB 70 PLHA 73

RESULT 15  
US-10-046-801-15  
; Sequence 15, Application US/10046801  
; Patent No. 6808720  
; GENERAL INFORMATION:  
; APPLICANT: Unger, Evan C.  
; TITLE OF INVENTION: Charged Lipids and Uses For The Same  
; FILE REFERENCE: UNGR1592  
; CURRENT APPLICATION NUMBER: US/10/046,801  
; CURRENT FILING DATE: 2002-05-13  
; PRIOR APPLICATION NUMBER: US/09/540,448  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 08/925,353  
; PRIOR FILING DATE: 1997-09-08  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 73  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. 6808720el Sequence

US-10-046-801-15

Query Match 86.1%; Score 329; DB 4; Length 73;  
Best Local Similarity 82.8%; Pred. No. 1e-25;  
Matches 53; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDAATCKLTGSGCADGLCCDQCFMKEGTVCRRAGDDLDDYCNGISAGCPN 61  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 10 SPANPCDAATCKLPGAGCGEGLCCDQCFMKEGTICRRAGDDLDDYCNGISAGCPN 69

QY 62 PFHA 65  
|||||  
DB 70 PLHA 73

Search completed: November 3, 2005, 08:20:24  
Job time : 43 secs

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**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:14:38 / Search time 169 Seconds  
(without alignments)  
160.927 Million cell updates/sec

Title: US-10-712-584-2\_COPY\_419\_483

Perfect score: 382

Sequence: 1 DAPANPCDDAATCKLTGSGO.....DUDYCNIGISACPRNPFHA 65

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep:\*
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- 18: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubppaa/US11\_PUBCOMB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*
- 21: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*
- 22: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382	100.0	483	US-10-439-532-2	Sequence 2, Appli
2	382	100.0	483	US-10-712-584-2	Sequence 2, Appli
3	346	90.6	73	US-10-089-473A-10	Sequence 10, Appli
4	345	90.3	73	US-10-089-473A-1	Sequence 1, Appli
5	334	87.4	73	US-09-813-484-15	Sequence 15, Appli
6	334	87.4	73	US-10-439-532-9	Sequence 9, Appli
7	334	87.4	73	US-10-712-584-9	Sequence 9, Appli
8	332	86.9	73	US-09-776-268A-1	Sequence 1, Appli
9	329	86.1	73	US-10-046-801-15	Sequence 15, Appli
10	322	84.3	552	US-10-439-532-8	Sequence 8, Appli
11	322	84.3	552	US-10-712-584-8	Sequence 8, Appli

12	321.5	84.2	71	10	US-09-832-501-37	Sequence 37, Appli
13	321.5	84.2	71	14	US-10-439-532-7	Sequence 7, Appli
14	321.5	84.2	71	16	US-10-712-584-7	Sequence 7, Appli
15	286	74.9	478	14	US-10-078-866-2	Sequence 2, Appli
16	266	69.6	73	14	US-10-439-532-10	Sequence 10, Appli
17	266	69.6	73	16	US-10-712-584-10	Sequence 10, Appli
18	265	69.4	111	9	US-09-921-823-23	Sequence 23, Appli
19	265	69.4	111	9	US-09-921-823-8	Sequence 8, Appli
20	261	68.3	71	15	US-10-383-588A-6	Sequence 6, Appli
21	261	68.3	463	15	US-10-383-588A-2	Sequence 2, Appli
22	261	68.3	481	15	US-10-383-588A-8	Sequence 8, Appli
23	258	67.5	69	9	US-09-813-484-14	Sequence 14, Appli
24	244	63.9	70	9	US-09-813-484-17	Sequence 17, Appli
25	244	63.9	70	14	US-10-046-801-17	Sequence 17, Appli
26	243	63.6	69	14	US-10-046-801-14	Sequence 14, Appli
27	241.5	63.2	70	10	US-09-961-656-9	Sequence 9, Appli
28	238.5	62.4	68	14	US-09-813-484-16	Sequence 16, Appli
29	238.5	62.4	68	14	US-10-046-801-16	Sequence 16, Appli
30	228	59.7	68	14	US-10-439-532-11	Sequence 11, Appli
31	228	59.7	68	16	US-10-712-584-11	Sequence 11, Appli
32	228	59.7	478	16	US-10-439-532-14	Sequence 14, Appli
33	228	59.7	478	16	US-10-712-584-14	Sequence 14, Appli
34	223	58.4	400	9	US-09-921-823-2	Sequence 2, Appli
35	219	57.3	611	9	US-09-921-823-17	Sequence 17, Appli
36	214	56.0	616	18	US-10-482-925A-1	Sequence 18, Appli
37	207.5	54.3	76	10	US-09-877-843-88	Sequence 88, Appli
38	199	52.1	606	14	US-10-439-532-12	Sequence 12, Appli
39	199	52.1	606	16	US-10-712-584-12	Sequence 12, Appli
40	197	51.6	282	9	US-09-840-277-109	Sequence 109, Appli
41	195.5	51.2	571	14	US-10-439-532-13	Sequence 13, Appli
42	195.5	51.2	571	16	US-10-712-584-13	Sequence 13, Appli
43	191	50.0	49	9	US-09-840-277-8	Sequence 8, Appli
44	191	50.0	49	15	US-10-360-101-92	Sequence 92, Appli
45	191	50.0	49	20	US-11-066-697-1132	Sequence 1132, Appli

## ALIGNMENTS

RESULT 1  
US-10-439-532-2  
/ Sequence 2, Application US/10439532  
/ Publication No. US20030186884A1  
GENERAL INFORMATION:  
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA  
TITLE OF INVENTION: CORTICOSTERIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST.  
FILE REFERENCE: 1279-338N2/09801388  
CURRENT APPLICATION NUMBER: US/10/439,532  
CURRENT FILING DATE: 2003-05-16  
PRIOR APPLICATION NUMBER: US09/591,552  
PRIOR FILING DATE: 2000-06-08  
NUMBER OF SEQ ID NOS: 15  
/ SOFTWARE: PatentIn version 3.1  
/ SEQ ID NO 2  
/ LENGTH: 483  
/ TYPE: PRT  
/ ORGANISM: Agkistrodon contortrix  
US-10-439-532-2

Query Match 100.0%; Score 382; DB 14; Length 483;  
Best Local Similarity 100.0%; Pred. No. 6.1e-32;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 DAPANPCDDAATCKLTGSGCAGDGCQCKFMKEGIVCRARGGDLDDYCNIGISACPR 60
DB	419 DAPANPCDDAATCKLTGSGCAGDGCQCKFMKEGIVCRARGGDLDDYCNIGISACPR 478
QY	61 NPFHA 65
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RESULT 2
US-10-712-584-2
; Sequence 2, Application US/10712584
; Publication No. US20040132659A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; APPLICANT: Markland, Francis S.
; APPLICANT: Riteer, Matthew
; TITLE OF INVENTION: CONTORTOSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; FILE REFERENCE: 1279-338N3/09801388
; CURRENT APPLICATION NUMBER: US/10/712,584
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US09/591,552
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 08/141,321
; PRIOR FILING DATE: 1993-10-22
; PRIOR APPLICATION NUMBER: US 08/540,423
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: US 08/632,691
; PRIOR FILING DATE: 1996-04-15
; PRIOR APPLICATION NUMBER: US 08/745,603
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: US09/460,295
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PR
; ORGANISM: Agkistrodon contortrix
US-10-712-584-2

Query Match          100.0%; Score 382; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 6,1e-32;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  DAPNPCCDAATCKLTTSQCADGLCCDDCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 60
DB      419 DAPNPCCDAATCKLTTSQCADGLCCDDCKFMKEGTVCRRARGDDLDDYCNGISAGCPR 478

QY      61 NPFA 65
DB      479 NPFA 483

RESULT 3
US-10-089-473A-10
; Sequence 10, Application US/10089473A
; Publication No. US20050032189A1
; GENERAL INFORMATION:
; APPLICANT: CHUNG, Kwang-Hoe
; APPLICANT: KIM, Doo-Sik
; APPLICANT: KOH, You-Seok
; APPLICANT: SOHN, Young-Dong
; APPLICANT: YOU, Meon-Kyoo
; APPLICANT: JANG, Yang-Soo
; APPLICANT: HUH, Chin-Kyu
; TITLE OF INVENTION: NOVEL PROTEIN DERIVED FROM AGKISTRODON SAXATILIS EMELIANOV AND PR
; FILE REFERENCE: 0136/0K432US0
; CURRENT APPLICATION NUMBER: US/10/089,473A
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 73
; TYPE: PR
; ORGANISM: Agkistrodon halys brevicaudus
US-10-089-473A-10
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QY      62 PFHA 65
DB      70 PFHA 73

RESULT 4
US-10-089-473A-1
; Sequence 1, Application US/10089473A
; Publication No. US20050032189A1
; GENERAL INFORMATION:
; APPLICANT: CHUNG, Kwang-Hoe
; APPLICANT: KIM, Doo-Sik
; APPLICANT: KOH, You-Seok
; APPLICANT: SOHN, Young-Dong
; APPLICANT: YOU, Meon-Kyoo
; APPLICANT: JANG, Yang-Soo
; APPLICANT: HUH, Chin-Kyu
; TITLE OF INVENTION: NOVEL PROTEIN DERIVED FROM AGKISTRODON SAXATILIS EMELIANOV AND PR
; FILE REFERENCE: 0136/0K432US0
; CURRENT APPLICATION NUMBER: US/10/089,473A
; CURRENT FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 73
; TYPE: PR
; ORGANISM: Agkistrodon saxatilis emelianov
US-10-089-473A-1

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Best Local Similarity 87.5%; Pred. No. 8,8e-29;
Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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DB      10  APNPCCDAATCKLRGAQACAGLCCDDCKFMKEGTICRMARGDDMDYCNGISAGCPRN 69

QY      62 PFHA 65
DB      70 PFHA 73

RESULT 5
US-09-813-484-15
; Sequence 15, Application US/09813484
; Publication No. US20010031243A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Filled Compositions
; FILE REFERENCE: UNGR1600
; CURRENT APPLICATION NUMBER: US/09/813,484
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 08/929,847
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 73
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-09-813-484-15
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Query Match      87.4%; Score 334; DB 9; Length 73;
Best Local Similarity 84.4%; Pred. No. 1.3e-27;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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      10 SPANPCCDATCKLTPGAGCGEGLCCDQCSFMKKGITCRARDDLDYCNGISAGCCPN 69
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      62 PFHA 65
      :|||
      70 PLHA 73

Db

RESULT 6
US-10-439-532-9
; Sequence 9, Application US/10439532
; Publication No. US20030186884A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; TITLE OF INVENTION: CONTOPTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338N2/09801388
; CURRENT APPLICATION NUMBER: US/10/439,532
; PRIOR FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US09/591,552
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Trimeresurus albolabris
US-10-439-532-9

Query Match      87.4%; Score 334; DB 14; Length 73;
Best Local Similarity 84.4%; Pred. No. 1.3e-27;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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      62 PFHA 65
      :|||
      70 PLHA 73

Db

RESULT 7
US-10-712-584-9
; Sequence 9, Application US/10712584
; Publication No. US20040132659A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
; APPLICANT: Markland, Francis S.
; APPLICANT: Ritzer, Matthew
; TITLE OF INVENTION: CONTOPTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
; TITLE OF INVENTION: OTHER CONDITIONS
; FILE REFERENCE: 1279-338N3/09801388
; CURRENT APPLICATION NUMBER: US/10/712,584
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US09/591,552
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 08/141,321
; PRIOR FILING DATE: 1993-10-22
; PRIOR APPLICATION NUMBER: US 08/540,423
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: US 08/632,691
; PRIOR FILING DATE: 1996-04-15
; PRIOR APPLICATION NUMBER: US 08/745,603
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: US 09/163,047
; PRIOR FILING DATE: 1998-09-29
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; PRIOR APPLICATION NUMBER: US09/460,295
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Trimeresurus albolabris
US-10-712-584-9

Query Match      87.4%; Score 334; DB 16; Length 73;
Best Local Similarity 84.4%; Pred. No. 1.3e-27;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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      10 SPANPCCDATCKLTPGAGCGEGLCCDQCSFMKKGITCRARDDLDYCNGISAGCCPN 69
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      62 PFHA 65
      :|||
      70 PLHA 73

Db

RESULT 8
US-09-776-268A-1
; Sequence 1, Application US/09776268A
; Publication No. US20010023242A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Doo-Sik
; APPLICANT: CHUNG, Kwang Hoe
; APPLICANT: KANG, In-Cheol
; TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
; FILE REFERENCE: 0136/1P733-US1
; CURRENT APPLICATION NUMBER: US/09/776,268A
; PRIOR FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: US 09/335,088
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: KR 99-20579
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: KR 98-23778
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Agkistrodon halys breviceaudus
US-09-776-268A-1

Query Match      86.9%; Score 332; DB 9; Length 73;
Best Local Similarity 84.4%; Pred. No. 2e-27;
Matches 54; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      2 APANPCCDATCKLTGSGCAGDLCCDQCKFMKEGTVCRARDDLDYCNGISAGCCPN 61
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      10 SPANPCCDATCKLTPGAGCGEGLCCDQCSFMKKGITCRARDDLDYCNGISAGCCPN 69
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      62 PFHA 65
      :|||
      70 PLHA 73

Db

RESULT 9
US-10-046-801-15
; Sequence 15, Application US/10046801
; Publication No. US20030054027A1
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/10/046,801
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/540,448
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/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 08/925,353
/ PRIOR FILING DATE: 1997-09-08
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 15
/ LENGTH: 73
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: No. US20030054027A1 Sequenc
US-10-046-801-15

Query Match
Best Local Similarity 86.1%; Score 329; DB 14; Length 73;
Matches 53; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARGDDLDYCNIGISAGCPRN 61
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DB 10 SPANPCDDAATCKLFGAQCGBGLCCDQCSFMKGTICRRARGDDLDYCNIGISAGCPRN 69

QY 62 PFHA 65
:|||||
DB 70 PFHA 73

RESULT 10
US-10-439-532-8
/ Sequence 8, Application US/10439532
/ Publication No. US20030186884A1
/ GENERAL INFORMATION:
/ APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
/ TITLE OF INVENTION: CONTOFROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
/ FILE REFERENCE: 1279-338N2/09801388
/ CURRENT FILING DATE: 2003-05-16
/ PRIOR APPLICATION NUMBER: US09/591,552
/ PRIOR FILING DATE: 2000-06-08
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 552
/ TYPE: PRF
/ ORGANISM: Trimeresurus gramineus
US-10-439-532-8

Query Match
Best Local Similarity 84.3%; Score 322; DB 14; Length 552;
Matches 53; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARGDDLDYCNIGISAGCPRN 61
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DB 489 SPANPCDDAATCKLFGAQCGBGLCCDQCSFMKEGTVCRARGDDLDYCNIGISAGCPRN 548

QY 62 PFHA 65
:|||||
DB 549 PFHA 552

RESULT 11
US-10-712-584-8
/ Sequence 8, Application US/10712584
/ Publication No. US20040132659A1
/ GENERAL INFORMATION:
/ APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
/ APPLICANT: Markland, Francis S.
/ APPLICANT: Rietter, Matthew
/ TITLE OF INVENTION: CONTOFROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
/ FILE REFERENCE: 1279-338N3/09801388
/ CURRENT APPLICATION NUMBER: US/10/712,584
/ CURRENT FILING DATE: 2003-11-12
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/ PRIOR APPLICATION NUMBER: US09/591,552
/ PRIOR FILING DATE: 2000-06-08
/ PRIOR APPLICATION NUMBER: US 08/141,321
/ PRIOR FILING DATE: 1993-10-22
/ PRIOR APPLICATION NUMBER: US 08/540,423
/ PRIOR FILING DATE: 1995-10-10
/ PRIOR APPLICATION NUMBER: US 08/632,691
/ PRIOR FILING DATE: 1996-04-15
/ PRIOR APPLICATION NUMBER: US 08/745,603
/ PRIOR FILING DATE: 1996-11-08
/ PRIOR APPLICATION NUMBER: US 09/163,047
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: US09/460,295
/ PRIOR FILING DATE: 1999-12-10
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 552
/ TYPE: PRF
/ ORGANISM: Trimeresurus gramineus
US-10-712-584-8

Query Match
Best Local Similarity 84.3%; Score 322; DB 16; Length 552;
Matches 53; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARGDDLDYCNIGISAGCPRN 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 489 SPANPCDDAATCKLFGAQCGBGLCCDQCSFMKEGTVCRARGDDLDYCNIGISAGCPRN 548

QY 62 PFHA 65
:|||||
DB 549 PFHA 552

RESULT 12
US-09-832-501-37
/ Sequence 37, Application US/09832501
/ Publication No. US20030199043A1
/ GENERAL INFORMATION:
/ APPLICANT: Ballance, David J.
/ APPLICANT: Sleep, Darrell
/ APPLICANT: Turner, Andrew J.
/ APPLICANT: Sadegh, Homa
/ APPLICANT: Prior, Christopher P.
/ TITLE OF INVENTION: Albumin Fusion Proteins
/ FILE REFERENCE: PF542
/ CURRENT APPLICATION NUMBER: US/09/832,501
/ CURRENT FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: 60/229,358
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: 60/256,931
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/199,384
/ PRIOR FILING DATE: 2000-04-25
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 37
/ LENGTH: 71
/ TYPE: PRF
/ ORGANISM: Agkistrodon piscivorus
US-09-832-501-37

Query Match
Best Local Similarity 84.2%; Score 321.5; DB 10; Length 71;
Matches 54; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

QY 2 APANPCDDAATCKLTGSGCAGDLCCDCKFMKEGTVCRARGDDLDYCNIGISAGCPRN 61
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DB 10 SPANPCDDAATCKLFGAQCAGDLCCDCKFMKEGTVCRARGDDLDYCNIGISAGCPRN 68

QY 62 PFH 64
:|||||
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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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